Sequence Diversity, Evolution and Transmission of Influenza A(H1N1)pdm09 and A(H3N2) Viruses in Kenya, 2009-2018

Thesis

SEQUENCE DIVERSITY, EVOLUTION, AND TRANSMISSION OF INFLUENZA A(H1N1)pdm09 AND A(H3N2) VIRUSES IN KENYA, 2009-2018

Thesis submitted for the award of degree of Doctor of Philosophy

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KEMRI | Wellcome Trust

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DECLARATION

This thesis describes my work, which I undertook at the Kenya Medical Research Institute (KEMRI)-Wellcome Trust Research Programme (KWTRP) under the supervision of Prof. D. James Nokes, Dr. Sandra S. Chaves, and Dr. Charles N. Agoti in fulfilment of the requirements for the degree of Doctor of Philosophy at the Open University (UK). I confirm that the dissertation is the result of my own work and does not contain anything that is the outcome of work done in collaboration. This work has not been submitted at any other university or institution for any other qualification.

Collection of samples and consenting was conducted as part of larger integrated studies on the surveillance of respiratory viruses. First, surveillance in Kilifi based on acute respiratory infection (ARI) in the Kilifi Health and Demographic Surveillance System (KHDSS) run by KWTRP in coastal Kenya. Second, surveillance across Kenya based on national severe acute respiratory infection (SARI) surveillance run by the Kenyan Ministry of Health and supported by the USA Centres for Disease Control and Prevention (CDC). Lastly, surveillance within Africa based on Pneumonia Etiology Research for Child Health (PERCH) study, which was run by the PERCH study group from 2011 to 2013. Sequence data for influenza viruses were generated at KWTRP (Kilifi, Kenya).

David Collins Owuor

Kilifi (Kenya), August 2020

ABSTRACT

Background

The global surveillance of human influenza viruses has resulted in the generation of a uniquely extensive collection of geographically and temporally comprehensive virus sequence data, which has provided an opportunity to explore the drivers behind the global spread of influenza viruses. However, due to the insufficient spatiotemporally representative virus sequence data from tropical and sub-tropical African countries, especially from sub-Saharan Africa, relatively little is known about the possible role these regions play in the global spread of influenza viruses. Using influenza A(H1N1)pdm09 virus and A(H3N2) virus sequence data, this study aimed to understand how seasonal influenza viruses are introduced and spread across geographically defined regions, whether local, national, continental or global, and their patterns of persistence across these regions.

Methods

A laboratory method for whole-genome sequencing (WGS) of influenza A(H1N1)pdm09 and A(H3N2) viruses on Illumina next-generation sequencing (NGS) platform was established at Kilifi, coastal Kenya. This was then used to sequence samples collected between 2009 and 2018 from geographically defined regions: local community in Kilifi (n=66); countrywide in Kenya (n=383); and across Africa from 5 countries (n=100). The arising genomes were analyzed using phylogenetic and phylogeographical methods to investigate the patterns of spread, persistence and fade-out of seasonal influenza viruses at a local community in Kilifi, countrywide in Kenya, and across the African continent. Additionally, a global contemporaneous sequence dataset was analyzed in conjunction with the WGS data from this study in a Bayesian framework for inference of the situation of sub-Saharan Africa in the global network of spread of influenza viruses.

Results

A total of 549 new influenza type A virus (IAV) whole genomes were generated during this study; 414 A(H1N1)pdm09 virus and 135 A(H3N2) virus genomes. Phylogeographical analyses revealed that local seasonal community epidemics of IAV were initiated by multiple independent introductions into the community, with each introduction commonly spreading to multiple locations within a relatively short period of time. Countrywide, in Kenya, circulation of IAV was predominantly characterized by virus migration from multiple locations to multiple destinations within the country and between locations in proximity; persistence of IAV countrywide might therefore be modulated by frequent virus introductions from outside the country and virus spread between locations in proximity. Continentwide, strains of IAV from Africa fell into strongly supported multinational lineages that suggested possible intra-continental spread of influenza viruses within Africa, which exhibited a significant northern to southern hemisphere migration. Globally, significant migration pathways from multiple geographical regions to multiple geographical destinations that also includes Africa were observed, which suggests that the seeding of epidemics of influenza viruses globally is driven by different geographical regions that also includes Africa. However, East or Southeast (E-SE) Asia acted as the major source of spread of influenza viruses globally, which is consistent with findings from other studies on the global circulation of influenza viruses. A greater global migration was observed for A(H3N2) virus compared to A(H1N1)pdm09 virus, consistent with greater global migration of A(H3N2) virus compared to A(H1N1)pdm09 virus.

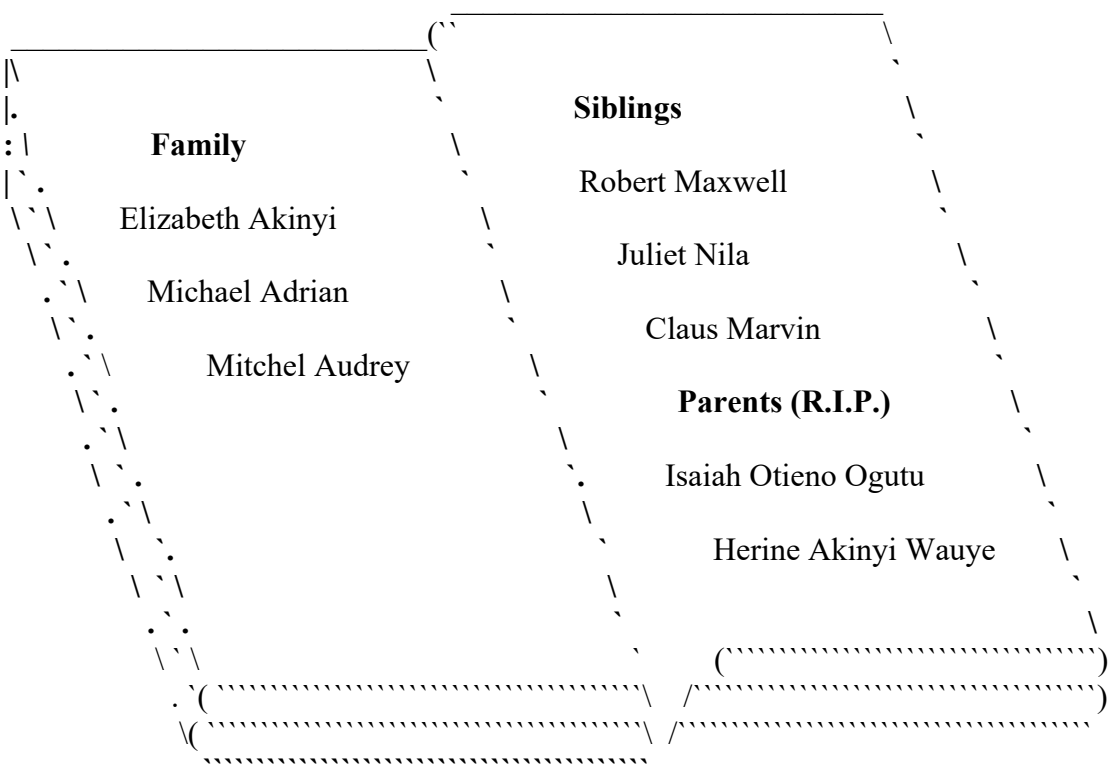
Conclusions

The global migration dynamics of seasonal influenza viruses are well understood, and several models have been proposed to describe these patterns. However, analysis of virus sequence data

from understudied regions, as exemplified in this study, suggests that these migration patterns are far more complex than those proposed by current models alone. For example, the findings from this study support the notion that influenza viruses persist as temporally structured migrating metapopulations in which new virus strains can emerge in any geographical region, including in Africa, with the location of the source population changing regularly. The epidemics across geographically defined regions (local community, countrywide, continentwide, and globally) are also interconnected at various scales of observation to different extents. Therefore, a more complete understanding of the global migration dynamics of influenza viruses requires deeper and wider sampling of viruses from understudied tropical and sub-tropical regions, notably, Africa, South and Central Asia, and South America. Understanding the circulation patterns of influenza viruses across geographically defined regions, together with their origins and patterns of persistence, is useful in selecting the most effective vaccine strains for the circulating seasonal influenza viruses. The rapid and widespread global mixing of viruses from all northern and southern hemisphere countries including in countries in Africa, Asia, Europe, North America, South America, and Oceania as reported in this study emphasize that global vaccine recommendations need well distributed, widespread global influenza A(H1N1)pdm09 virus and A(H3N2) virus sampling from as many localities as possible.

DEDICATION

This thesis is dedicated to:



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To my Supervisors, James, Sandra, and Charles, “Thank You!”.

A special appreciation to James who sparked an interest in me to pursue a PhD when he presented the work done by his Virus Epidemiology and Control (VEC) team at the 4th Medical and Veterinary Research conference in 2015. I am now completing my PhD with his prestigious team!

To Sandra, whose leadership at the Influenza Division, CDC, Kenya Country office (CDC-Kenya) created a research collaboration with the USA CDC, Influenza Genomics team, which was important for the success of my PhD. Asante!

To my PhD “desk mates”: Thank you for sharing this amazing journey with me.

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IDeAL Team: Sam, Dorcas, Liz, Rita, Florence, Solomon and David; Asante for the good work!

My Rotary family in Kilifi: Thank you for giving me the opportunity to serve the Kilifi community!

Family: Liz, Adrian, and baby Audrey, thank you for being the best “running mates” for my PhD candidature.

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LIST OF ABBREVIATIONS

ALRI	Acute lower respiratory illness
ARI	Acute respiratory infection
BAM	Binary Alignment Map
BaTS	Bayesian Tip-association Significance
BEAST	Bayesian Evolutionary Analysis Sampling Trees
BF	Bayes factor
BIC	Bayesian Information Criterion
BWT	Burrows-Wheeler transform
BSSVS	Bayesian stochastic search variable selection
CDC-Kenya	Centers for Disease Control and Prevention, Kenya Country office
Ct	Cycle threshold
E-SE	East or Southeast
GiRaF	Graph-incompatibility-based Assortment Finder
GISAID	Global Initiative on Sharing All Influenza Data
GISRS	Global Influenza Surveillance and Response System
IAV	Influenza type A Virus
ILI	Influenza-like illness
IRMA	Iterative Refinement Meta-Assembler
KEMRI	Kenya Medical Research Institute
KHDSS	Kilifi Health and Demographic Surveillance System
KNH	Kenyatta National Hospital
KWTRP	KEMRI-Wellcome Trust Research Programme
MCC	Maximum Clade Credibility
MoPHS	Kenyan Ministry of Public Health and Sanitation
M-RTPCR	Multi-segment reverse transcription-polymerase chain reaction
NGS	Next-generation sequencing
NIC	National Influenza Center
NP/OP	Nasopharyngeal and oropharyngeal
PCR	Polymerase chain reaction
PERCH	Pneumonia Etiology Research for Child Health

PopART	Population Analysis with Reticulate Trees
rRT-PCR	Real time reverse transcription polymerase chain reaction
SAM	Sequence Alignment Map
SARI	Severe acute respiratory illness
SERU	Scientific and Ethics Review Unit
SPREAD	Spatial Phylogenetic Reconstruction of EvolutionAry Dynamics
SPReD	Studying the Pathways of Respiratory virus Disease transmission
TCS	Templeton, Crandall and Sing
UK	United Kingdom
USA	United States of America
USAMRD-K	USA Army Medical Research Directorate, Kenya
VEC	Virus Epidemiology and Control
VTM	Viral transport medium
WHO	World Health Organization
WGS	Whole-genome sequencing

CHAPTER ONE

1 Background

1.1 Introduction

Influenza viruses are members of the genus *Influenzavirus* within the family *Orthomyxoviridae*. Epidemics of influenza have been recorded since 427 BC (Langmuir et al., 1985), with the most devastating occurring in the 1918 pandemic (worldwide epidemic), which is estimated to have resulted in 100 million deaths worldwide (Johnson and Mueller, 2002). The first human IAV was recovered in 1933 from patients with influenza (Smith et al., 1933). Sequencing of RNA fragments from tissue samples taken from 1918 pandemic victims allowed reconstruction of the extinct 1918 influenza pandemic virus (Taubenberger et al., 2005; Tumpey et al., 2005). Influenza type B and C viruses were first isolated in 1940 and 1947, respectively (Francis, 1940; Francis et al., 1950). Influenza type D virus was recently identified as a new genus, with reservoirs in pigs and cattle (Chiapponi et al., 2016; Hause et al., 2014). The first crude inactivated, monovalent human influenza vaccines were introduced in the early 1940s, which were followed by more purified, less reactogenic ones (Barberis et al., 2016a; Parodi et al., 2011). Large studies were later conducted in December 1942 that provided the first official proof that inactivated influenza vaccines could yield effective protection against influenza epidemics (Barberis et al., 2016b; Francis et al., 1945). Despite the availability of improved influenza vaccines and antivirals, seasonal influenza remains an important public health problem (Iuliano et al., 2018; Paget et al., 2019).

1.2 Influenza Disease Burden

Influenza virus is an important cause of acute lower respiratory illness (ALRI), which is a leading cause of morbidity and mortality worldwide (Iuliano et al., 2018; Lafond et al., 2016; Paget et al.,

2019; Simonsen et al., 2013). Persons of any age can be infected with influenza virus but children under the age of 5 years, the elderly persons aged ≥65 years and older, pregnant women, and individuals with chronic medical and immunosuppressive conditions are at increased risk of severe disease or complications when infected (Lafond et al., 2016; Paget et al., 2019; Simonsen et al., 2013; World Health Organization, 2018a). Healthcare workers are known to be at an increased risk of influenza virus infection due to increased exposure to the patients and risk further spread to vulnerable individuals (World Health Organization, 2018a).

A recent global study (2019) by Paget *et al.,* reported that there were an average of 389,000 (uncertainty range [UR] 294,000-518,000) influenza-virus-associated respiratory deaths globally each year, which corresponded to ~2% of all annual respiratory deaths between 2002 and 2011 (excluding the 2009 pandemic year); 67% of these deaths were reported among people aged ≥65 years (Paget et al., 2019). In children under 5 years of age globally, influenza was associated with 109.5 million influenza virus episodes (UR 63.1-190.6 million), 10.1 million influenza-virus-associated ALRI cases (6.8-15.1 million), 870,000 influenza-virus-associated ALRI admissions (543,000-1,415,000), 15,300 in-hospital deaths (5,800-43,800), and up to 34,800 (13,300-97,200) influenza-virus-associated ALRI deaths (Wang et al., 2020). Most of the influenza-virus-associated disease burden is in the developing countries (Gessner et al., 2011; Katz et al., 2012b; Ng and Gordon, 2015; Paget et al., 2019; Simonsen et al., 2013; Wang et al., 2020). In Kenya, the adjusted incidence rates of hospitalizations with influenza among children aged ≤5 years range from 2.7-4.7 per 1,000 (5.7 per 1,000 in children under the age ≤6 months), which are 7-10 times higher compared to persons aged ≥5 years (Emukule et al., 2015).

1.3 Influenza Genome Structure and Composition

Influenza A, B, C, and D virus types, which are 4 of 7 members of the *Orthomyxoviridae* family,

are enveloped, negative-sense, single-stranded RNA viruses with segmented genomes (Hayden and Palese, 2017; Shaw and Palese, 2013) of approximately 13,600 nucleotides in length (Ghedin et al., 2005). IAV and influenza B virus each possess 8 viral RNA (vRNA) segments, which can encode at least 11 different proteins: the non-structural proteins (NS1 and NS2), polymerase complex proteins (PB1, PB2, PA, PB1-related PB1-F2 and PB1 N40), matrix proteins (M1 and M2) and the surface glycoproteins (hemagglutinin (HA) and neuraminidase (NA)); influenza C and D viruses lack an NA gene thus only have 7 vRNA segments that can encode at least 9 different proteins (Bouvier and Palese, 2008; Hayden and Palese, 2017). Each vRNA segment contains conserved noncoding regions of different lengths at both the 5'- and 3'-ends. The extreme terminal 12 to 13 nucleotides at both the 5'- and 3'-ends of vRNAs are highly conserved among all genome segments of IAV (Bouvier and Palese, 2008). These highly conserved ends are then followed by a segment-specific noncoding region. A schematic representation showing the genome organization of influenza is shown in *Figure 1.1* (Shaw and Palese, 2013).

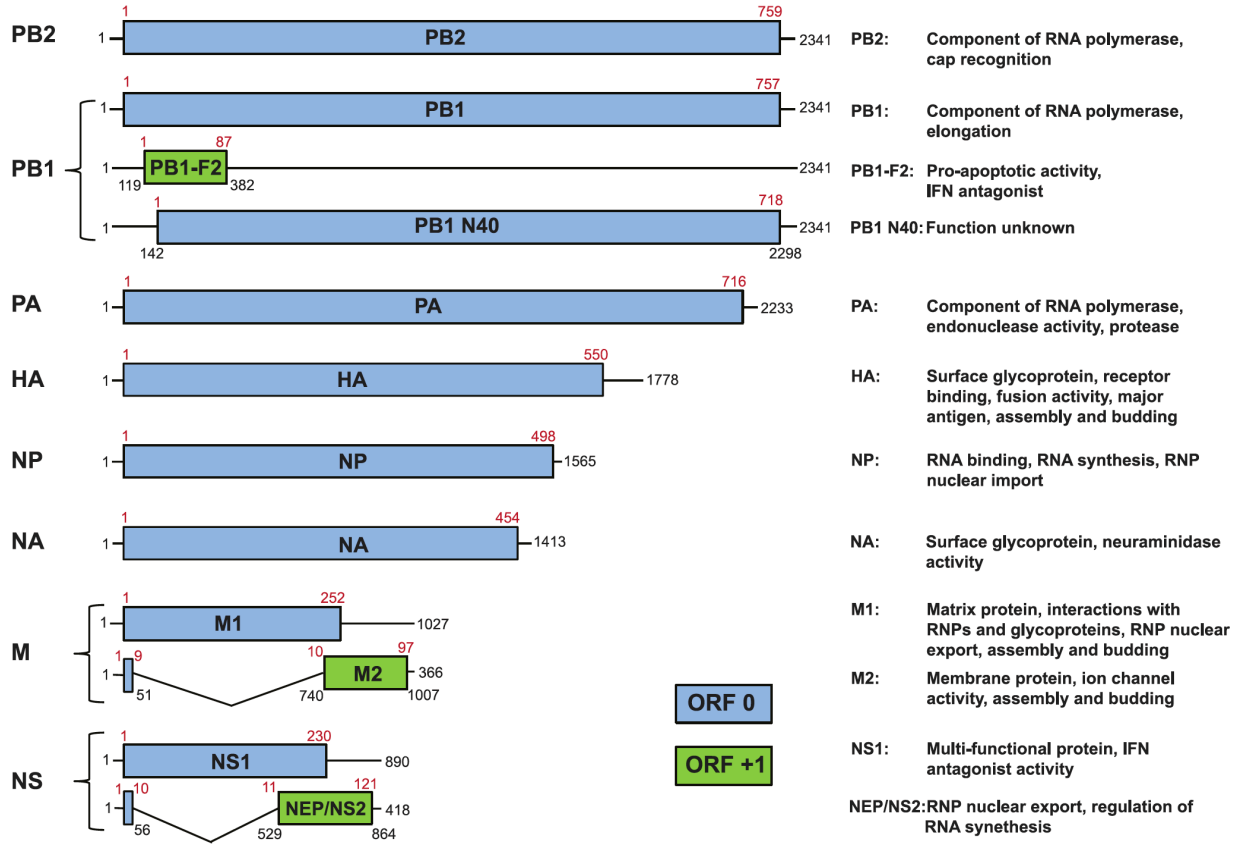


Figure 1.1: Schematic representation of influenza A/Puerto Rico/8/34 virus adopted from (Shaw and Palese, 2013). The segments are numbered in order of decreasing length. The size of each RNA segment is shown (nucleotides in black) shown in the positive sense and their encoded proteins (amino acids in red). Lines at 3'- and 5'-termini represent noncoding regions. Alternative splice variants are indicated with corresponding open reading frame (ORF), for example, PB1 segment's second and third ORFs in +1 and 0 frames result in PB1-F2 and PB1 N40 proteins, respectively. Introns are indicated by V-shaped lines. The role of each encoded protein is summarized at the segment ends.

1.4 Virion Structure

Influenza virus particles exist as either spherical or filamentous particles, which consist of segmented nucleocapsids surrounded by a lipid envelope that is covered with HA and NA glycoproteins (Bouvier and Palese, 2008; Shaw and Palese, 2013). The matrix M2 protein is also found in the lipid envelope of the virus, which overlay a matrix of M1 protein that encloses the virion ribonucleoprotein (RNP) core (Bouvier and Palese, 2008; Hayden and Palese, 2017; Krammer et al., 2018). The core consists of 8 RNA segments that are associated with one to several copies of viral polymerase complex proteins (PB1, PB2, and PA) surrounded by viral nucleoprotein (NP) molecules (Bouvier and Palese, 2008; Hayden and Palese, 2017; Krammer et al., 2018). *Figure 1.2* shows a cartoon structure of an influenza virus particle.

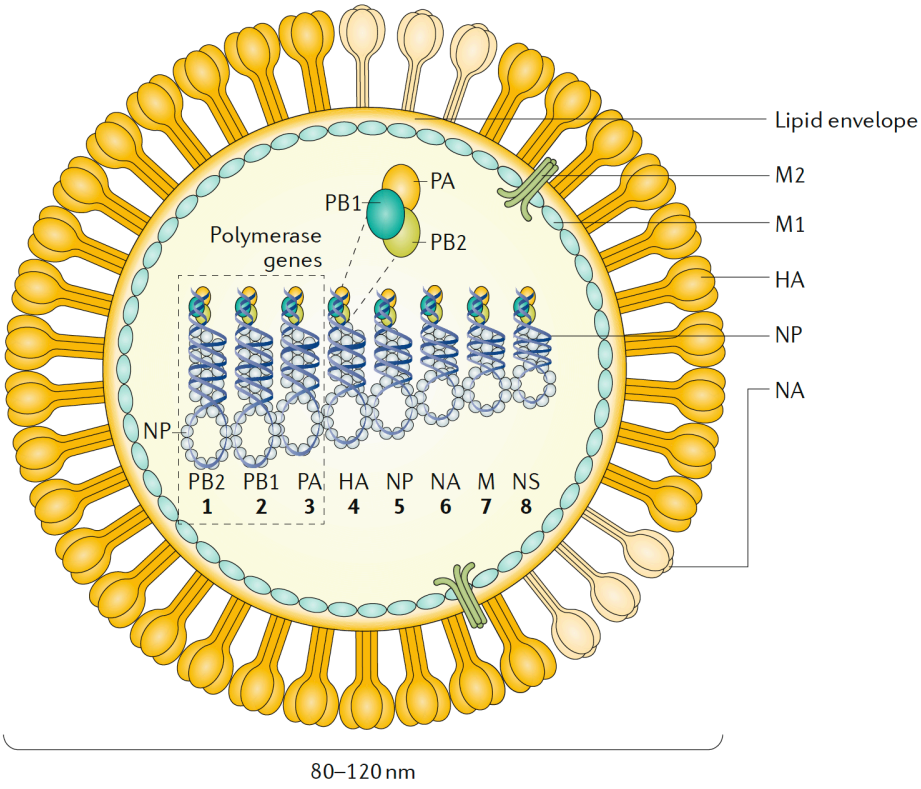


Figure 1.2: Influenza virion structure adopted from (Krammer et al., 2018) showing virion structural components.

1.5 Influenza Virus Classification

Influenza A, B, and C virus types are classified based on the antigenic properties of 2 major structural proteins: NP and matrix M1 protein (Hayden and Palese, 2017; Shaw and Palese, 2013). Infections by strains within these three types can be associated with classical influenza symptoms in humans (Hayden and Palese, 2017). A novel influenza D virus has been proposed as the fourth virus type within the genus *Influenzavirus* (Collin et al., 2015; Hause et al., 2014). IAV are further classified into antigenically diverse subtypes based on antigenic properties and gene sequences of two of their most antigenically variable proteins, HA and NA (Bouvier and Palese, 2008; Hayden and Palese, 2017). A total of 18 antigenically different HA (H1-H18) and 11 antigenically different NA (N1-N11) subtypes have been described for circulating IAV (Dutch et al., 2015; Tong et al., 2013). However, only 3 HA subtypes (H1, H2, and H3) and 2 NA subtypes (N1 and N2) have caused extensive outbreaks in humans (Hayden and Palese, 2017). The HA subtypes can be further subdivided into 2 groups based on the phylogeny of the HA molecule; *Figure 1.3*. Within each group, the domain encoding the HA stalk is antigenically similar (Krammer et al., 2018). Influenza B and C viruses are not divided into subtypes and are almost exclusively restricted to humans with no known animal reservoirs although limited spillover to wildlife has been reported for influenza B virus (Bodewes et al., 2013). Influenza B viruses have recently diverged (in early 1970s) into 2 antigenically distinct lineages (B/Victoria/2/1987-like and B/Yamagata/16/1988-like), which currently co-circulate in humans with 2 seasonal IAV subtypes: A(H1N1)pdm09 virus and A(H3N2) virus, respectively (Klimov et al., 2012).

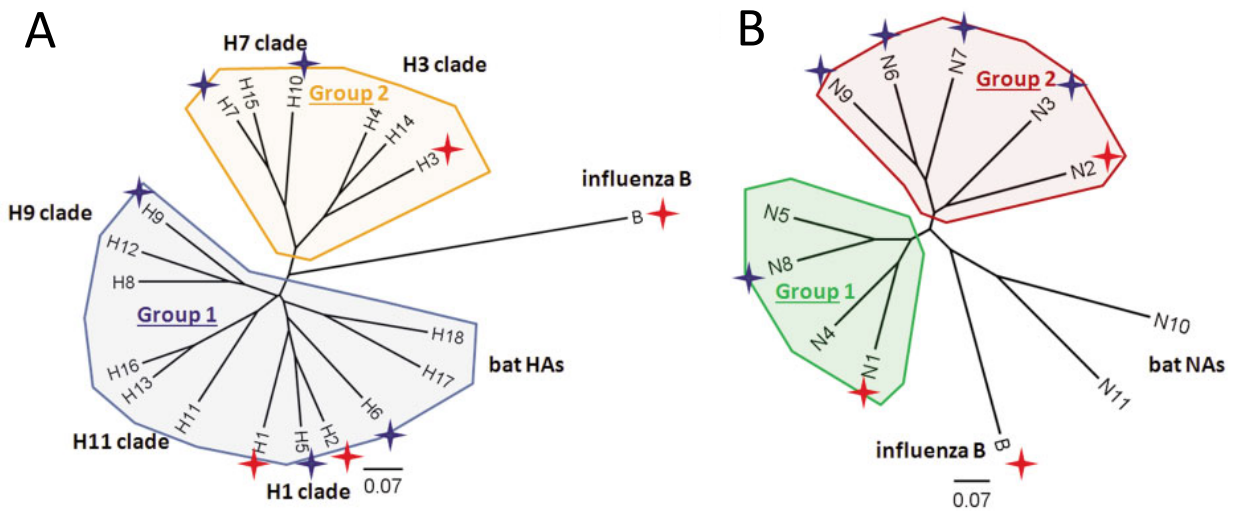


Figure 1.3: Phylogenetic tree of influenza virus HA (**A**) and influenza virus NA (**B**). Twelve HA subtypes (including two bat HAs) constitute group 1 (blue group) whereas 6 HA subtypes constitute group 2 (orange group). Influenza B virus only has 1 HA type (no subtype). Four NA subtypes constitute group 1 (green group) IAV NAs, while 5 are in group 2 (red group). The bat NAs (N10 and N11) and the influenza B virus NA (no subtypes) are evolutionarily divergent. The scale represents a 7% change in amino acid differences (From (Krammer et al., 2018); adapted, courtesy of Creative Commons Attribution Licensing). IAV, influenza A virus; HA, hemagglutinin; NA, neuraminidase.

The standard nomenclature for naming influenza virus strains includes: virus type; species from which the virus was isolated (omitted if human); location of isolation; isolate number; year of isolation; and, for IAV only, the antigenic description of HA and NA subtype in parenthesis (Bouvier and Palese, 2008; Shaw and Palese, 2013). For example, A/California/07/2009 (H1N1) was the seventh isolate of a human IAV isolated in California in 2009, with an HA subtype 1 and an NA subtype 1.

1.6 Influenza Virus Evolution

The annual recurrence of seasonal influenza epidemics is attributed to the continued evolution of seasonal influenza viruses (Krammer et al., 2018; Shaw and Palese, 2013). First, influenza viruses evolve through accumulation of nucleotide mutations, and if these result in changes to the amino acids in the HA and NA proteins (particularly in the antigenic sites), then the antigenicity of the strain will be altered in a process referred to as antigenic drift (Smith et al., 2004; Webster et al., 1992; Westgeest et al., 2012). These antigenic changes, especially in HA, result in escape from antibody-mediated immunity induced by previous infection or vaccination and allows the virus to re-infect individuals who were once immune to the virus (Webster et al., 1992). These changes also necessitate frequent updates of seasonal influenza virus vaccine formulations to ensure sufficient antigenic relatedness between the vaccine and emerging virus variants (Salk and Suriano, 1949; Tricco et al., 2013). Antigenic drift enables the continued circulation of influenza viruses in human populations and makes their behavior unpredictable (Smith et al., 2004). Antigenic drift periodically results in the emergence of new antigenic variants, which appear every 3-5 years for A(H3N2) virus and 3-8 years for A(H1N1) and influenza B viruses (Bedford et al., 2015; Smith et al., 2004; Vijaykrishna et al., 2015).

Influenza clades are assigned based on amino acid clade-defining substitutions in HA, for example, characterization of seasonal influenza A(H1N1)pdm09 and A(H3N2) viruses into genetic groups (i.e., clades, subclades, and subgroups) based on European CDC Guidelines (https://www.ecdc.europa.eu/en/seasonal-influenza/surveillance-and-disease-data/influenza-virus-characterisation). The clades are typically assigned using in-house scripts that is often paired with phylogenetic analyses to account for mismatched or missing amino acids among the clade-defining amino acids (Eisler et al., 2020). However, generating these clade definitions is

challenging, for example, through parallel evolution in which identical substitutions arising in different clades can confuse phylogeny algorithms into grouping distinct clades based on parallel mutations (Bedford et al., 2019). Therefore, several computational workflows and pipelines for assigning clades have been developed to standardize influenza virus clade assignment that include: Nextstrain, which is a visualization tool for sequence data with pre-established clade definitions for influenza (Hadfield et al., 2018); Influenza Classification Suite, which is a Galaxy workflow for rapid clade assignment (Eisler et al., 2020); and PhyCLIP, which uses linear integer programming to assign sequences into clades (Han et al., 2019).

Second, influenza viruses evolve through antigenic shift, which involves marked changes in HA and NA of IAV strains due to acquisition of new HA and NA gene segments from an influenza virus of a different subtype that may occur when a host is co-infected with influenza viruses (Bouvier and Palese, 2008; Westgeest et al., 2014). The resulting virus may encode completely novel antigenic proteins to which the human population has little or no preexisting immunity and which, if efficiently transmitted from person to person, can lead to pandemics (Bouvier and Palese, 2008; Hayden and Palese, 2017). Additionally, influenza virus reassortment, which involves the interchange of internal protein-coding genomic RNA segments when 2 viruses of the same type (that is, 2 IAV or 2 influenza B viruses) infect the same cell occurs due to the segmented nature of the influenza virus genome (Westgeest et al., 2014). A unique characteristic of IAV is the wide range of mammalian and avian species in which the viruses circulate that includes humans, domestic animals, pigs, horses, poultry, bats, and wild migratory birds (including >100 species of ducks, geese, gulls, and wild aquatic birds) among others (Krammer et al., 2018; Tong et al., 2013). The ability of IAV to populate nonhuman species has important epidemiological consequences, for example, the presence of an animal reservoir enables the virus to circulate outside humans such

that eradication of human IAV by immunization of humans is less likely (Krammer et al., 2018). Additionally, animal reservoirs of IAV provide a source of antigenically diverse HA and NA genes that can readily be exchanged by reassortment between viral strains after co-infection of the same host, which increases virus diversity and in some instances results in generation of human pandemic influenza virus strains whose HA and/or NA genes have been derived from animal strains (Hayden and Palese, 2017; Krammer et al., 2018; Shaw and Palese, 2013). Intersubtypic reassortments between avian, swine, and/or human IAV have led to several pandemics that have resulted in the emergence of novel viruses against which the human population has limited or nonexistent immunity, and which have efficiently been transmitted among humans, eventually becoming established as seasonal influenza viruses causing annual epidemics (Krammer et al., 2018; Taubenberger and Morens, 2010). For example, the 1957 A(H2N2) influenza pandemic emerged as a result of a reassortant A(H2N2) virus arising from the reassortment of the then circulating seasonal A(H1N1) virus and an avian A(H2N2) virus, which caused annual epidemics until 1968 when the A(H3N2) influenza pandemic emerged (Kilbourne, 2006; Taubenberger and Morens, 2010). The 1968 pandemic was a result of a reassortant A(H3N2) virus of a human A(H2N2) virus with an avian influenza A(H3N2) virus and has been a major cause of influenza epidemics since then, with significant morbidity and mortality (Kilbourne, 2006; Stöhr, 2002; Taubenberger and Morens, 2010; Westgeest et al., 2014). Reassortment between influenza viruses of the same subtype (intrasubtypic reassortment) also results in increased virus diversity, which shapes the short-term evolution of influenza viruses (Holmes et al., 2005; Nelson et al., 2008; Rambaut et al., 2008).

1.7 Influenza A(H1N1)pdm09 Virus

A novel influenza A(H1N1)pdm09 virus emerged in the Americas during March-April 2009,

spread rapidly among humans, and developed into the first human pandemic of the 21st century (CDC, 2009b; Dawood et al., 2009; Fraser et al., 2009; Garten et al., 2009; Gatherer, 2009; Smith et al., 2009). Influenza A(H1N1)pdm09 virus is a reassortant virus composed of PB2 and PA segments from the North American swine triple-reassortant lineage, NA and M segments from the Eurasian swine lineage, a human H3N2-like PB1 segment, and HA, NP, and NS segments from the classical swine lineage (Dawood et al., 2009; Garten et al., 2009; Smith et al., 2009). The virus was associated with the pandemic that was declared by the World Health Organization (WHO) in June 2009 (World Health Organization, 2010). The influenza A(H1N1)pdm09 virus host and lineage origins are shown in *Figure 1.4*.

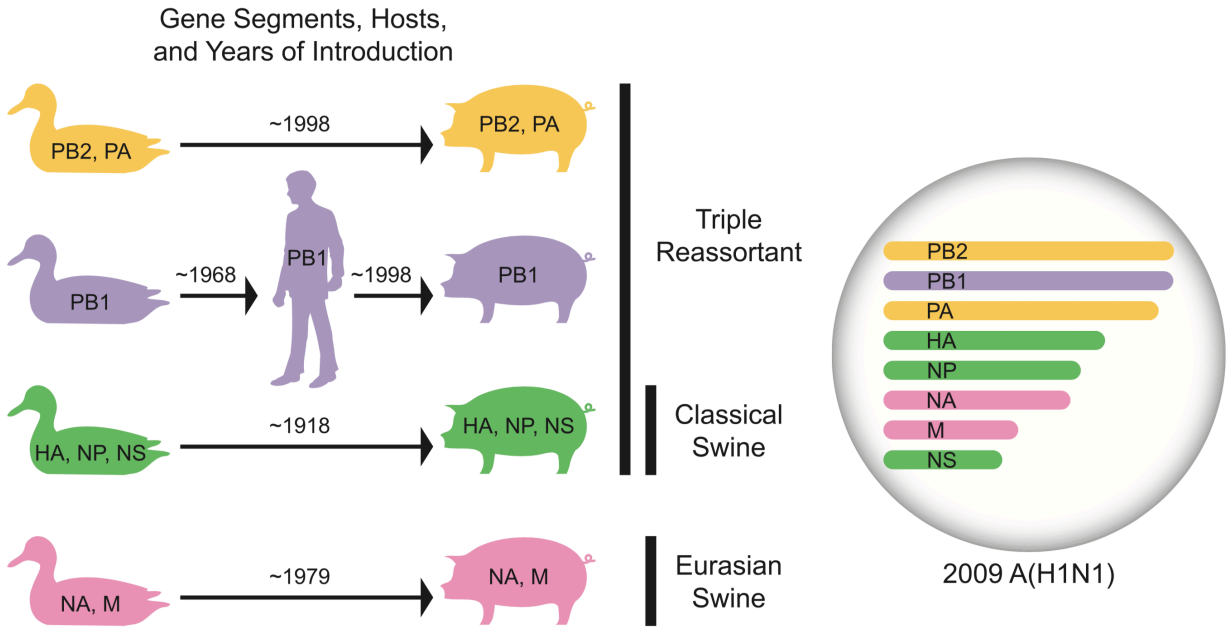
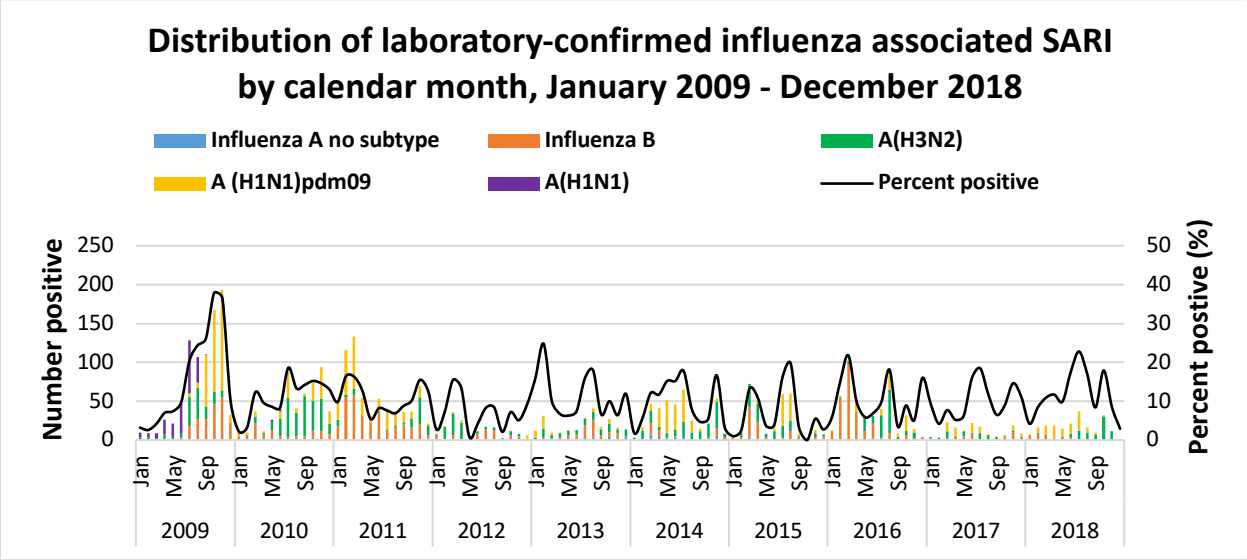


Figure 1.4: Influenza A(H1N1)pdm09 virus host and lineage origins adopted from (Garten et al., 2009) showing a representation of the 8 reassortant virus genome segments color-coded by host of origin.

The early transmission and spread of A(H1N1)pdm09 virus was rapid with 168 countries reporting infections by July 2009; this was associated with 162,300 laboratory-confirmed cases globally and over 1,100 human deaths during the early phase of the pandemic (Nelson et al., 2009; Rambaut and Holmes, 2009; World Health Organization, 2010). A modelling study (2012) by Dawood *et al.* estimated that there were 201,200 respiratory deaths (range 105,700-395,600) and an additional 83,300 cardiovascular deaths (range 46,000-179,900) associated with the 2009 A(H1N1)pdm09 virus pandemic; 80% of the respiratory and cardiovascular deaths occurred in people aged ≤65 years with 51% of these deaths occurring in Southeast Asia and Africa (Dawood et al., 2012). Following this period, A(H1N1)pdm09 virus has caused seasonal epidemics and has co-circulated with influenza A(H3N2) and influenza B viruses in most countries (Baillie et al., 2012; Nelson et al., 2011; Su et al., 2015; Vijaykrishna et al., 2015) having replaced seasonal A(H1N1) virus that had circulated in humans for over 32 years from 1977 to 2009 (Kilbourne, 2006). Kenya reported her first case of A(H1N1)pdm09 virus on June 29, 2009, sentinel surveillance activities identifying 4 separate introductions into the country that quickly spread countrywide with infections peaking in November 2009 and later becoming the dominant circulating influenza virus (CDC, 2009a; Katz et al., 2014; Osoro et al., 2011); *Figure 1.5*.



Abbreviations: SARI, severe acute respiratory illness.

Figure 1.5: Temporal patterns of influenza A and B viruses as observed through the National Influenza Sentinel Surveillance detections in Kenya between January 2009 and December 2018 (Source: Centers for Disease Control and Prevention, Kenya office (CDC-Kenya) influenza surveillance data accessed 13 January 2020). The first y axis indicates monthly counts of influenza A(H1N1)pdm09 virus indicated by a yellow bar, influenza A(H1N1) virus indicated by a purple bar, influenza A(H3N2) virus indicated by a green bar, influenza B virus indicated by an orange bar, and non-subtyped IAV indicated by a blue bar. The percent influenza virus positives by month between January 2009 and December 2018 is indicated by the black continuous line in the second y axis. The introduction of A(H1N1)pdm09 virus into Kenya in 2009, its dominance and outcompeting of seasonal A(H1N1) virus, and most recent seasonal occurrence is also shown. IAV, influenza A virus; SARI, severe acute respiratory illness.

1.8 Investigating Influenza A(H1N1)pdm09 Virus in the Genomics Era

Influenza A(H1N1)pdm09 virus being responsible for the first pandemic in the genomic era, with over 2,000 virus genomes generated during 2009-2010 alone, provided a unique opportunity to investigate the emergence and establishment of a novel pathogen in humans across different spatiotemporal scales of observation, particularly in regions with comprehensive virological surveillance, defined chronology of epidemic waves, and disease surveillance (Su et al., 2015). This offered an opportunity to explore the global spread of a novel virus and investigate different transmission models including local spread and virus introductions from outside a locality in the dissemination of infections in a community. Most important for my work, investigation of the emergence and establishment of A(H1N1)pdm09 virus in the Kenyan population is important in understanding how the virus was introduced into the local population and the nature and pace of spread in the population at different scales of observation: from the local community, for example, Kilifi, Kenya to across the country, and from the African continent to worldwide.

Until recently, only partial HA, NA, and M gene segment changes of circulating human seasonal influenza virus strains were tracked routinely through partial sequencing (World Health Organization, 2019a). These were used to track influenza evolution (HA and NA) and antiviral drug resistance (NA and M), which was coupled with hemagglutinin inhibition assay (antigenic characterization of influenza virus) to identify new vaccine strains. However, the emergence and detection of highly pathogenic avian influenza A(H5N1) virus caused a rapid expansion in surveillance efforts for zoonotic viruses to the extent that sequencing of all gene segments of avian and swine viruses is now routine (World Health Organization, 2019a). Since antigenic drift and shift events create virus strains that may not be efficiently captured in the host immune responses generated by current influenza vaccines, it is important to track the changes in all gene segments

during surveillance of circulating influenza virus strains (Taubenberger and Morens, 2010; Westgeest et al., 2014). Although partial sequence data (HA and NA) provide useful information regarding antigenic evolution of the virus, they often lack adequate phylogenetic resolution required to infer spatial dynamics at particular localized scales (Viboud et al., 2013). For example, segments other than HA can harbor different phylogeographical patterns due to frequent reassortment events essential in development of genetic diversity and drug resistance (Viboud et al., 2013). Individual gene segments may also have differing internal mutation rates and independent evolutionary histories due to reassortment (Westgeest et al., 2014). Additionally, mutations that are associated with mammalian adaptation of IAV also occur in multiple gene segments of the virus genome, thus identification of these mutations can provide insights into the likelihood of an influenza virus adapting to a new host (World Health Organization, 2019a).

The availability of partial and whole-genome virus sequence data enabled investigations into the emergence and establishment of A(H1N1)pdm09 virus in the human population (Dawood et al., 2009; Fraser et al., 2009; Garten et al., 2009; Smith et al., 2009) and its ongoing evolution including genetic and antigenic drift, and reassortment (Baillie et al., 2012; Nelson et al., 2009; Su et al., 2015; Westgeest et al., 2014). For example, early phylogenetic studies utilized partial (HA and NA gene sequences) and concatenated WGS data to investigate the emergence and diversification of A(H1N1)pdm09 virus (Dawood et al., 2009; Fraser et al., 2009; Garten et al., 2009; Rambaut and Holmes, 2009; Smith et al., 2009). The analysis revealed that distinct genetic virus clades arose early during the pandemic and disseminated globally, which was associated with global co-circulation of 7 phylogenetically distinct A(H1N1)pdm09 virus clades (clades 1 through 7). These clades were geographically dispersed and displayed extensive spatial and temporal mixing (Baillie et al., 2012; Dawood et al., 2009; Garten et al., 2009; Nelson et al., 2009).

Additionally, clade 7 viruses were found to be the most diverse and became globally dominant with the diversity attributed to continuous antigenic drift and its predominance attributed to better fitness, adaptability, and highly efficient transmissibility (Nelson et al., 2009; Smith et al., 2009; Su et al., 2015). In Kenya, phylogenetic analyses of concatenated WGS data identified an initial introduction of global clade 2 and 7 A(H1N1)pdm09 viruses into the country but clade 2 viruses did not circulate beyond the introduction foci whereas clade 7 viruses disseminated countrywide (Gachara et al., 2016). However, there are insufficient studies, which have utilized partial and WGS data to investigate the emergence, establishment, and ongoing evolution of A(H1N1)pdm09 virus in Africa (Byarugaba et al., 2016; Dia et al., 2013; Gachara et al., 2016; Nelson et al., 2014; Venter et al., 2012) despite the high disease burden, especially in the sub-Saharan Africa region (Gessner et al., 2011; Katz et al., 2012b; Ng and Gordon, 2015).

The emergent A(H1N1)pdm09 virus rapidly replaced the seasonal A(H1N1) virus that had circulated in humans from 1977 to 2009 (Kilbourne, 2006). However, the mechanisms behind influenza strain replacement in humans is not fully understood (Su et al., 2015). Notably, A/California/07/2009 (H1N1)pdm09-like virus had been the recommended WHO vaccine strain for inclusion into the seasonal influenza vaccine for both the southern and northern hemisphere recommendations from 2010 to 2017, which indicates that the emergent lineage had not undergone significant antigenic changes despite causing several seasonal influenza epidemics since its emergence (World Health Organization, 2015). The recommended vaccine strain has since been updated three times: to A/Michigan/45/2015 (H1N1)pdm09-like virus for the 2017/18 and 2018/19 influenza seasons (World Health Organization, 2018b); to A/Brisbane/02/2018 (H1N1)pdm09-like virus for the 2019/20 influenza season (World Health Organization, 2019b); and to A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like virus for the 2020/21 influenza

season egg-based vaccine (World Health Organization, 2020b). Therefore, this provides an opportunity to investigate the mechanisms behind influenza strain replacement in humans.

1.9 Viral Phylodynamics – Basic Concepts

The ability of a pathogen to survive and reproduce in one host and spread to a new host determines its success or failure (Bliven and Maurelli, 2016). Selective pressures which shape the genomes of microbial populations are exerted by host immune systems, predators, microbial competitors, parasites and environmental resource limitations (Toft and Andersson, 2010). Grenfell *et al.* coined the term "phylodynamics" to refer to the melding of immunodynamics, epidemiology, and evolutionary biology (Grenfell et al., 2004), *Figure 1.6*. Pathogen evolution is usually characterized by accumulation of genetic variation, which is modulated by host immunity, transmission bottlenecks, and epidemic dynamics (Wille and Holmes, 2020). The current study aimed to infer the local and global molecular epidemiological dynamics of IAV in Kenya within this phylodynamic framework.

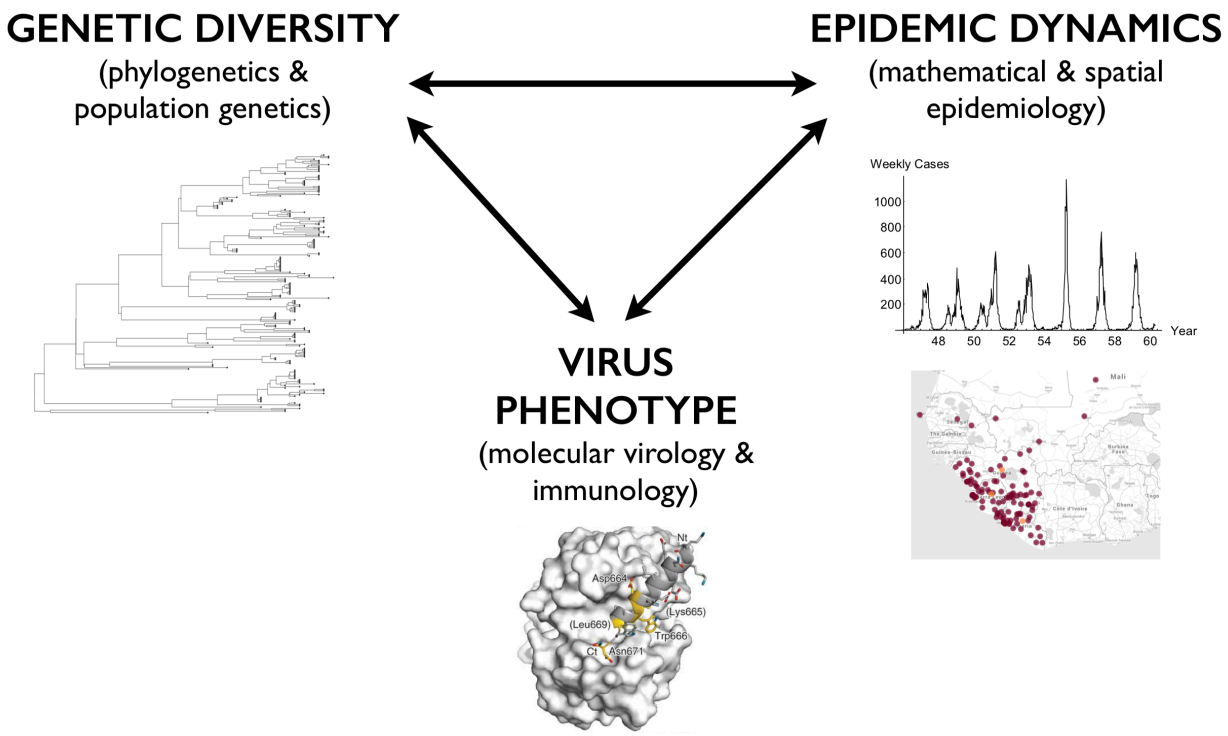


Figure 1.6: A representation of the components of viral phylodynamics adopted from (Pybus, 2016).

Phylodynamic data is composed of gene or genome sequence data, which have been sampled at different time points and from different geographical locations. These time points can be daily, weekly or monthly within single epidemics or over several epidemics (years). The geographical locations can be the subjects' residential areas, health care facilities, towns, cities, countries or continents (Lemey et al., 2009a; Pybus, 2016). Because of the corresponding timescale of evolutionary and spatial dynamics of spread, genetic sequence data in combination with other datasets may offer a valuable source of information to reconstruct the transmission of rapidly evolving pathogens such as emergent IAV (Holmes, 2008; Pybus and Rambaut, 2009). The increasingly complex quantitative phylodynamic approaches allow integration with the additional data types, for example, flight data in these analyses (Lemey et al., 2014; Lemey et al., 2009a).

1.9.1 Phylodynamics of Influenza A Viruses

Following its emergence in 2009, A(H1N1)pdm09 virus has caused seasonal epidemics and has co-circulated with A(H3N2) and influenza B viruses in most countries (Baillie et al., 2012; Nelson et al., 2011; Su et al., 2015; Vijaykrishna et al., 2015) including Kenya (Emukule et al., 2019; Katz et al., 2014). Influenza viruses that circulate in human populations differ in their evolutionary behavior (Bedford et al., 2014), which are reflected in their phylodynamic patterns: the structure of viral phylogenetic trees generated by a combination of evolutionary and epidemiological processes (Grenfell et al., 2004). Seasonal influenza A(H1N1)pdm09 and A(H3N2) viruses have markedly different dynamics (Bedford et al., 2015; Bedford et al., 2014; Vijaykrishna et al., 2015), *Figure 1.7*. Whereas A(H3N2) virus experiences a strongly selectively driven evolutionary pattern, which is associated with frequent selective sweeps, strong antigenic drift, and major seasonal bottlenecks in genetic diversity, A(H1N1)pdm09 virus experiences less common epidemics and selective sweeps, associated with persistence of multiple viral lineages across seasons (Rambaut et al., 2008; Vijaykrishna et al., 2015). These dynamics mirror the parallel patterns observed for the 2 influenza B virus lineages in which the Victoria lineage viruses undergo punctuated fluctuations in genetic diversity similar to A(H3N2) virus whereas the Yamagata lineage viruses experience fewer seasonal fluctuations, slower epidemics, and lower rates of amino acid changes even though multiple lineages persist across influenza seasons for both lineages (Bedford et al., 2014; Vijaykrishna et al., 2015), *Figure 1.7*. Possible explanations for these distinct patterns include differences in receptor-binding preferences that have been shaped by HA structure or the age structure of infected individuals, which also differs among influenza subtypes and likely impacts the cross-protective patterns of immunity (Bedford et al., 2015; Vijaykrishna et al., 2015). Additionally, population genetic analysis suggests that A(H1N1)pdm09 and A(H3N2) viruses

compete with each other resulting in the epidemic dominance of a single subtype (Vijaykrishna et al., 2015). Currently, there are efforts to use the phylogenetic patterns of influenza viruses to predict which virus variants will dominate in the future, and therefore should be incorporated into future vaccines, with online tools able to depict viral evolution in real time (Hadfield et al., 2018).

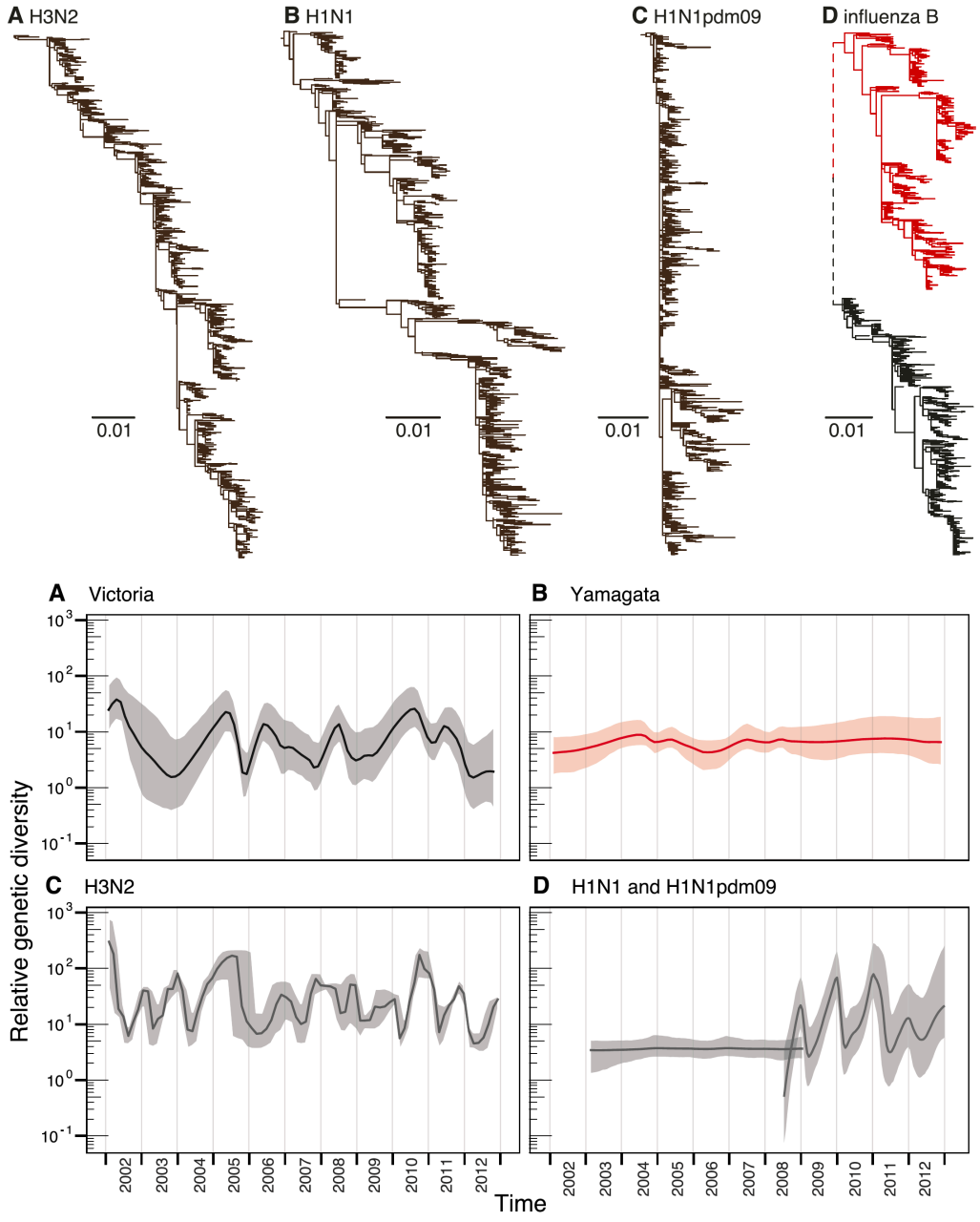


Figure 1.7: The contrasting phylodynamics of influenza viruses. *(Top) Left-to-right*: Phylogenetic trees of global HA genes of A(H3N2) virus, 2002–13; A(H1N1) virus, 1998–09; A(H1N1)pdm09 virus, 2009–13; and IBV Yamagata (red) and Victoria (black) lineages, 2002–13. Different tree shapes reflect the impact of differing evolutionary pressures. *(Bottom) Left-to-right*: Relative genetic diversities over time in IBV Victoria and Yamagata (orange) lineages; A(H3N2) virus; A(H1N1) virus; and A(H1N1)pdm09 virus using viruses sampled in Australia and New Zealand. (From (Vijaykrishna et al., 2015); adapted, courtesy of Creative Commons Attribution Licensing.) IAV, influenza A virus; IBV, influenza B virus.

1.10 Phylogeographical Inference in Virus Genomics

Phylogeography or phylogeographical methods enable inference of the geographical history of genetic lineages, which can elucidate the transmission dynamics of a given pathogen. Phylogeography requires availability of sequence data together with corresponding sampling location and sampling date to reconstruct the origin and spread of viruses (Baele et al., 2017; Lemey et al., 2009a; Pybus et al., 2015). A phylogeny with corresponding locations for the leaf nodes of the tree allows phylogeographic inference of locations for internal nodes of the tree, which reconstructs the source of outbreaks and subsequent routes of spread. The current stochastic models for phylogeography are based on Bayesian inference (Bloomquist et al., 2010; Faria et al., 2011; Lemey et al., 2009a). Discrete Bayesian phylogeography incorporates a continuous time Markov chain (CTMC) process to model transitioning among discrete location states throughout evolutionary history, which can be modelled as either symmetric or asymmetric transition (Lemey et al., 2009a). The symmetric substitution model specifies a discrete state ancestral state reconstruction using a standard CTMC, in which transition rates between locations are reversible whereas asymmetric substitution model specifies a discrete state ancestral state reconstruction using a nonreversible CTMC (https://beast.community/workshop_discrete_diffusion). Although similar to parsimonious approaches, which also map discrete character states onto phylogenetic trees by minimizing the number of changes between states as applicable for phylogeographic reconstruction, discrete trait inference with CTMC models is a more advanced approach for phylogeographic reconstruction compared to parsimonious approaches as it incorporates model uncertainty and branch lengths, generating posterior probabilities to evaluate the quality of the reconstruction (Lemey et al., 2009a). Therefore, the improved discrete trait inferences with CTMC models allow inference of the rates matrix of among-location transition states among discrete

locations; the rates matrix can be modelled using generalized linear model to test and quantify the contribution of a range of potential predictors of viral spread (Lemey et al., 2014). Bayesian phylogeography has been used to study influenza viruses (Bedford et al., 2015), HIV (Faria et al., 2014), Zika virus (Faria et al., 2017), and Ebola virus (Tong et al., 2015). However, these methods generally have several drawbacks. For example, due to the large number of parameters that are estimated in Bayesian phylogeographic studies, the analysis is slow for larger datasets and the number of distinct states is also limited (Reimering et al., 2020). Therefore, locations are often aggregated into larger regions such as continents (Bedford et al., 2015; Lemey et al., 2014) even though more finely resolved locations such as countries, states, cities, towns, and even villages are available for many sequences (Reimering et al., 2020). Additionally, since discrete Bayesian methods generally estimate rates of migration from the data, these methods will only infer observed locations, which excludes possible intermediate states that have not been sampled (Lemey et al., 2009a; Lemey et al., 2010; Reimering et al., 2020).

Continuous phylogeography, based on inference of geographic coordinates using Brownian random walk models in continuous space, is an alternative Bayesian phylogeography method to infer intermediate locations (Lemey et al., 2010). Although a good model for local spread of rapidly evolving viruses, it is less applicable for viruses that spread both locally and over large distances in very short periods of time, for example, by air travel in the case of influenza viruses (Reimering et al., 2020). Additionally, for both Bayesian inference methods, additional drawbacks include the effect of sampling biases on phylogeographic reconstructions as well as lack of sufficient strategies to mitigate the bias incorporated within the model parameters (Reimering et al., 2020). However, improvements to these existing phylogeographic methods have been proposed by overcoming the shortcomings inherent in their Bayesian inference models. For

example, a parsimony-based approach for phylogeographic reconstruction that overcomes the shortcomings of discrete Bayesian methods, which uses a unique algorithm that identifies internal locations; this minimize the distances along the phylogenetic tree and allows for the use of fine-grained locations and inference of intermediate locations (Reimering et al., 2020).

1.10.1 Phylogeography of Influenza A Viruses

The global surveillance of influenza viruses has resulted in the generation of a uniquely extensive collection of geographically and temporally comprehensive virus sequences, which has provided an opportunity to explore the drivers behind the global migration of influenza viruses (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2009b; Rambaut et al., 2008; Russell et al., 2008). Various epidemiological questions have been explored through phylogeographical analyses of sequence data of influenza viruses, for example, the existence of a source-sink model of global influenza circulation. In the model, countries have putative tropical sources of influenza viruses, which are characterized by year-round (or multi-annual) transmission, local persistence of influenza lineages, and relatively high genetic diversity of influenza viruses. It is then postulated that lineages of influenza viruses migrate and seed seasonal epidemics in cooler temperate regions, where they experience inter-seasonal extinction (Rambaut et al., 2008). Therefore, the epidemics in temperate climates are not typically sustained but are re-established by importation of virus lineages from populations with more persistent transmission in the tropics (Nelson et al., 2007; Rambaut et al., 2008; Russell et al., 2008).

Most of the analyses on the drivers of global circulation of influenza viruses, mainly aimed at elucidating the global source population of influenza viruses, have focused on E-SE, which is attributed in part due to the apparent origins of several pandemics and seasonal epidemics in E-SE Asia (Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2014; Russell et al., 2008). For

example, studies have shown that globally, annual A(H3N2) virus epidemics result from the introduction of new genetic variants from E-SE Asia, where viruses circulate via a network of temporally overlapping epidemics (Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2014; Russell et al., 2008) rather than local persistence (Nelson et al., 2007; Nelson et al., 2006; Rambaut et al., 2008; Russell et al., 2008). These studies that have aimed, for example, to infer the location through time of the 'source' population of A(H3N2) virus have concluded that the virus resides primarily in the E-SE Asia (Bedford et al., 2010; Kosakovsky Pond et al., 2010; Lemey et al., 2014; Russell et al., 2008). However, additional analyses of virus sequence data from temperate regions particularly the USA have revealed a considerable contribution of the temperate regions to the global virus population (Bahl et al., 2011; Bedford et al., 2010); evidence also exists for virus migration into Asia from elsewhere (Bahl et al., 2011; Bedford et al., 2015). The A(H3N2) virus studies suggest that the migration dynamics of A(H3N2) virus are far more complex than those represented by a simple source-sink model alone. Therefore, a more complete understanding of the global circulation dynamics of influenza viruses requires deeper and wider sampling from understudied tropical and sub-tropical regions (Viboud et al., 2013). For example, additional analysis of recently generated sequence data of influenza viruses from India led to the discovery that the global source region for A(H3N2) virus also includes India in addition to E-SE Asia (Bedford et al., 2015), which highlights the importance of additional sequence data from understudied localities. Because of the insufficient spatiotemporally representative sequence data of influenza viruses from tropical and sub-tropical African countries, especially from sub-Saharan Africa, relatively little is known about the possible role the region plays in the global spread of influenza viruses (Byarugaba et al., 2016; Dia et al., 2013; Gachara et al., 2016; Nelson et al., 2014). No study has reported an in-depth phylogeographical analysis of Kenyan (local and

countrywide) and African spread of influenza viruses and the role of Africa in the global migration dynamics of influenza viruses. The current study aimed to investigate the role of Africa in the global migration dynamics of IAV using spatiotemporal sequence data from Kenya, additional sequence data from Mali, The Gambia, Zambia, and South Africa, and publicly available contemporaneous sequence data from other African countries.

1.11 Whole-Genome Sequencing of Influenza A Viruses

The segmented nature of IAV RNA genome makes it technically challenging to obtain full genome coverage since the individual segments have to be amplified simultaneously. Reverse transcription PCR (RT-PCR), to amplify each of the 8 genomic RNA segments, is stoichiometrically difficult to perform especially when starting with *ex vivo* specimens, for example, nasopharyngeal/oropharyngeal (NP/OP) swabs (Van den Hoecke et al., 2015). Until recently, only HA, NA, and M gene segment changes of circulating human seasonal influenza virus strains were tracked routinely (World Health Organization, 2019a). Using next-generation sequencing (NGS), or high-throughput technologies, it is not only feasible but also routine to sequence all gene segments of most sampled seasonal influenza viruses, which generates full-length WGS data of influenza viruses (World Health Organization, 2019a). WGS provides comprehensive genetic information rather than HA and NA sequence alone, which improves the resolution of phylogenetic analyses, for example, to elucidate whether cases within an outbreak are clonal (Houghton et al., 2017; Meinel et al., 2018). Furthermore, WGS provides an even higher resolution than partial sequencing by informing on intra-host heterogeneity that may reveal additional clues on the direction of transmission when combined with epidemiological data, which may not be visible at the consensus level (Houghton et al., 2017).

Several factors have contributed to the increased use of NGS combined with bioinformatics for

influenza virus research and public health, which include increased availability of NGS platforms, lower costs of NGS platforms allowing WGS in real-time, reduced turnaround time both for sequencing and NGS data analysis, improvements in sequencing error rates (Goldstein et al., 2017; Lee et al., 2016; Maljkovic Berry et al., 2020; World Health Organization, 2019a), development of rapid portable sequencing technologies (Imai et al., 2018; Wang et al., 2015), for example, Oxford Nanopore Technology, and development of free, web-based access to bioinformatics software (Borges et al., 2018; Connor et al., 2016). Some NGS technologies also allow for deep sequencing, which not only provides for generation of simple consensus sequences but also enables the estimation of frequencies of both consensus and minority alleles with greater confidence due to the increased coverage depth that it provides (Rutvisuttinunt et al., 2013; Seong et al., 2016; Watson et al., 2013). However, challenges for setting up a high-quality NGS and bioinformatics laboratory capacity include the selection of the right sequencing platform, wet laboratory sequencing methods and bioinformatics tools, requirement for highly skilled personnel with high experience and expertise to generate accurate and informative results, and computational and information technology infrastructure to support the analyses of large amounts of data from NGS and bioinformatics (Gargis et al., 2016; Maljkovic Berry et al., 2020). Additionally, to keep NGS costs down, batching of samples is required, which results in longer turnaround times, for example, when needed to resolve transmission during outbreaks (Houghton et al., 2017). NGS is also limited to viral load with lower success rates in generating WGS data from samples with high cycle threshold (Ct) values (low viral load), for example, a Ct cut-off value of 32 for successful IAV NGS (Houghton et al., 2017) and other respiratory RNA viruses (Thorburn et al., 2015).

The commonest technology for influenza virus NGS is the Illumina platform (https://www.illumina.com/systems/sequencing-platforms.html). With 96 (up to 384) multiplexed

samples per run, the Illumina Nextera XT Sample Preparation Kit (https://www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/nextera-xt-dna.html) and Illumina MiSeq System (https://www.illumina.com/systems/sequencing-platforms/miseq.html) offer significantly higher throughput than conventional first-generation technologies, for example, Sanger (capillary electrophoresis) sequencing that is commonly used for influenza virus gene sequencing; thus, it is both cost-effective and efficient for sample processing (Deng et al., 2015; Houghton et al., 2017; Maljkovic Berry et al., 2020; Wang et al., 2015). The high data output (gigabytes) from NGS instruments allows sequencing of genomes of multiple influenza viruses, thus reducing the cost per genome compared to conventional approaches, for example, Sanger sequencing; depending on the technology, NGS also improves timeliness for sequencing a large number of samples (World Health Organization, 2019a). Although Sanger sequencing generates high quality, long reads, and is cost effective for small studies, it is labor-intensive, slow and not easily adapted for processing large numbers of samples, which also require high quality starting material to produce good-quality sequences (Deng et al., 2015; Maljkovic Berry et al., 2020; Wang et al., 2015). The Illumina Nextera XT kit is an amplicon-based NGS library preparation kit, which employs an enzymatic process to cleave DNA amplicons into fragments of approximately 300 base-pairs while integrating transposon sequences onto both 5'- and 3'-ends of the fragments; subsequent amplicon sequencing produces full-length sequences with even coverage from one end to the other with an optimized DNA library synthesis protocol (Illumina, 2020; Lee et al., 2016). Thus, the technology, also known as short-read sequencing, generates reads of up to 300 base-pairs, based on initial amplicon fragmentation and sequencing. The MiSeq is one of the most versatile platforms for NGS amongst the range of platforms from Illumina including GAIIx, MiSeqDx, NextSeq, NovaSeq, MiniSeq and iSeq

Systems (https://www.illumina.com/systems/sequencing-platforms.html). It has a fast run time of moderate cost per megabase and lower error rates compared with other NGS platforms, for example, Ion Torrent, Pacific Biosciences PacBioRS/RSII and MinION Systems. Additionally, the MiSeq is compact enough to fit on a standard laboratory bench and has a strong user support community (Maljkovic Berry et al., 2020). PacBioRS/RSII and MinION sequencers are high-throughput, long-read single molecule sequencers, which generate longer reads of approximately 10 kilobases but have higher single-pass sequencer error rates (14% and 13-20% for PacBioRS/RSII and MinION Systems, respectively) (Maljkovic Berry et al., 2020; Radford et al., 2012) that require complex error correction algorithms (Au et al., 2012). Therefore, the MiSeq is the system of choice for NGS and has been utilized successfully for IAV NGS in different clinical and research settings (Goldstein et al., 2017; Imai et al., 2018; Lakspere et al., 2014; Lee et al., 2016; Meinel et al., 2018; Rutvisuttinunt et al., 2013; Seong et al., 2016; Van den Hoecke et al., 2015; Wang et al., 2015; Wuthrich et al., 2019) most of which utilized the multi-segment RT-PCR (M-RTPCR) full-genome amplification technique for IAV (Zhou and Wentworth, 2012).

Although Sanger sequencing of HA1 region remains the most commonly used method for IAV characterization (Deng et al., 2015; Houghton et al., 2017) particularly by National Influenza Centers (NICs) globally (World Health Organization, 2019a), NGS is widely used, which often allows WGS directly from clinical specimens. The benefits of WGS (through NGS) over partial gene sequencing (through Sanger sequencing) for surveillance of influenza viruses include additional investigations on: influenza virus adaptation to a new host following its emergence (Su et al., 2015); virus reassortment events (Ghedin et al., 2005; Goldstein et al., 2017; Holmes et al., 2005); low-level virulence markers, minority variant populations (Ghedin et al., 2011; Ghedin et al., 2005; Van den Hoecke et al., 2015; Watson et al., 2013) and viral quasispecies (Meinel et al.,

2018; Van den Hoecke et al., 2015); tracking and predicting virus evolution, detecting emergence and establishment of new variants, and selecting vaccine strains (Belanov et al., 2015; Hedge et al., 2013); nosocomial outbreaks of influenza (Meinel et al., 2018; Seong et al., 2016); intra-host genetic diversification (Sobel Leonard et al., 2016; Xue et al., 2017); and detection of mixed infections and drug resistance (Ghedin et al., 2011; Rutvisuttinunt et al., 2013). Additionally, direct sequencing of viruses from clinical specimens reduces the time and costs involved in virus cell culture, allows for analysis of non-culturable virus strains, and avoids *in vitro* mutations which occur during virus propagation (Goldstein et al., 2017; Meinel et al., 2018). A summary of select IAV studies, which also show different NGS strategies employed is shown in *Table 1.1*.

Table 1.1: Influenza virus NGS studies showing the NGS sequencing strategy employed.

Study	Objective	NGS strategy
(Su et al., 2015)	Influenza virus adaptation to a new host following emergence; natural selection following adaptation.	Virus cell culture, RNA extraction, amplicon RT-PCR, and sequencing.
(Holmes et al., 2005)	Virus lineage co-circulation, persistence, and reassortment.	Virus cell culture, RNA extraction, amplicon RT-PCR, and sequencing.
(Watson et al., 2013)	Detection of minority variant population.	Virus cell culture, RNA extraction, amplicon multi-segment multi-step RT-PCR, and sequencing.
(Van den Hoecke et al., 2015)	Detection of minority variants and quasispecies.	Virus cell culture, RNA extraction, amplicon multi-segment RT-PCR, and sequencing.
(Rutvisuttinunt et al., 2013)	Simultaneous and complete genome sequencing of influenza A and B viruses.	Virus cell culture, RNA extraction, amplicon RT-PCR, and sequencing.
(Goldstein et al., 2017)	Direct sequencing of influenza viruses from clinical specimens and detection of reassortment events.	Direct RNA extraction from clinical specimen, amplicon multi-segment RT-PCR, and sequencing.
(Ghedin et al., 2011)	Detection of mixed infections and drug resistance.	Direct RNA extraction from clinical specimen, amplicon M-RTPCR, and sequencing.
(Meinel et al., 2018)	Investigation of nosocomial influenza virus outbreak and viral quasispecies during outbreaks.	Direct RNA extraction from clinical specimen, amplicon M-RTPCR, and sequencing.
(Seong et al., 2016)	Investigation of nosocomial influenza virus outbreak.	Direct RNA extraction from clinical specimen, amplicon M-RTPCR, and sequencing.

(Hoper et al., 2011)	Broad comprehensive deep sequencing using a novel amplicon target-capture technique.	Direct RNA extraction from clinical specimen, amplicon one- or two-step RT-PCR, and sequencing.
(Sobel Leonard et al., 2016)	Virus selective bottleneck and intra-host genetic diversification.	Direct RNA extraction from clinical specimen, amplicon M-RTPCR, and sequencing.
(Wang et al., 2015)	MinION nanopore sequencing of IAV genome and comparison with Illumina sequencing.	Direct RNA extraction from clinical specimen, amplicon M-RTPCR, and sequencing on Illumina and MinION sequencers.
(Imai et al., 2018)	MinION nanopore sequencing of influenza A and B viruses in a clinical setting and comparison with Illumina sequencing.	Direct RNA extraction from clinical specimen, amplicon M-RTPCR, and sequencing on Illumina and MinION sequencers.
(Xue et al., 2017)	Parallel evolution across multiple spatiotemporal scales; intra-host variant	Direct RNA extraction from clinical specimen, amplicon RT-PCR, and sequencing.

1.12 Surveillance of Respiratory Viruses in Kenya

Surveillance of multiple respiratory viruses is ongoing in several parts of Kenya (Katz et al., 2014; Nokes et al., 2009; Nyiro et al., 2018; Scott et al., 2012a). These are carried out by KEMRI, Ministry of Health, Kenya, KWTRP, CDC-Kenya, and the USA Army Medical Research Directorate, Kenya (USAMRD-K). In 2007, the Ministry of Health, Kenya with technical support from CDC-Kenya established a National Influenza Surveillance System in response to the 2005 influenza A(H5N1) virus threat. The aims of the surveillance system were to identify circulating strains of influenza virus, describe the epidemiology and burden of influenza in Kenya, and serve as a component of an early warning system for pandemic influenza (Katz et al., 2014). CDC-Kenya conducts surveillance for influenza and influenza-like illness (ILI) and SARI throughout the country (Emukule et al., 2014; Katz et al., 2014) in sentinel hospitals, health facilities at demographic surveillance sites, and refugee camps representing varied urban, rural, high mobility, and socio-economic conditions (Emukule et al., 2014; Katz et al., 2014). Surveillance activities are conducted in several sites including 1 referral hospital, Kenyatta National Hospital (KNH), 4 county and referral hospitals (Kakamega, Mombasa, Nakuru, and Nyeri), Kakuma refugee camp, and 3 Population Based Infectious Disease Surveillance (PBIDS) sites (Kibera, Lwak, and Siaya) (Breiman et al., 2015; Katz et al., 2014). Surveillance in Embu and Garissa county and referral hospitals were recently terminated in 2013 while Dadaab refugee camp was terminated in 2006 (Breiman et al., 2015; Feikin et al., 2011; Katz et al., 2014). The KWTRP VEC team established research collaboration with CDC-Kenya through a joint study and a countrywide pathways of transmission study entitled Studies of the Pathways of transmission of Respiratory virus Disease (SPReD-Kenya study) – (http://virec-group.org/spred-kenya/).

Research collaboration between KWTRP and 4 research and academic institutions in Africa conducted the PERCH-Africa study, which was a multi-country comprehensive case-control study in 5 African countries that aimed to evaluate the etiological agents causing severe or very severe childhood pneumonia in developing countries between 2011 and 2013. Availability of archived IAV samples from influenza surveillance in SPReD-KHDSS conducted by KWTRP enables the use of archived samples to understand the community spread of influenza viruses whereas availability of archived IAV samples from the CDC-Kenya and KWTRP-CDC-Kenya research collaboration enables the use of archived samples to understand the countrywide spread of influenza viruses. Additionally, availability of archived IAV samples from the PERCH-Africa study enables the use of archived samples to understand the continentwide spread of influenza viruses in Africa.

1.13 Justification/Contribution of the Proposed Study to Knowledge

IAV is an important cause of ALRI and a leading cause of morbidity and mortality worldwide. Children aged <5 years, individuals aged ≥65 years, pregnant women, and individuals with chronic medical and immunosuppressive conditions are at increased risk of severe disease or complications when infected (World Health Organization, 2018a). Safe and effective vaccines and antivirals exist; however, seasonal influenza viruses remain an important public health problem globally. The global migration dynamics of seasonal IAV are well understood, and various models have been proposed to describe these patterns on a global scale. However, additional data from understudied regions suggest that these migration patterns are far more complex than those proposed by current models alone. Therefore, a more complete understanding of the global migration dynamics of influenza viruses requires deeper and wider sampling of viruses from understudied tropical and sub-tropical regions, for example, sub-Saharan Africa. An opportunity

exists to better characterize the migration dynamics of influenza viruses at various scales of observation (local community, countrywide, continentwide, and worldwide), which are favored by three factors: (i) the emergence and introduction of a novel A(H1N1)pdm09 virus into the continent, the country, and the local community, whose samples were collected and archived in the SPReD-Kenya and PERCH-Africa studies, and the availability of archived A(H3N2) virus samples from the SPReD-KHDSS and PERCH-Africa studies; (ii) availability of high-throughput sequencing technologies for virus NGS, which generates high quality virus sequence data; and (iii) developments in high computing bioinformatics capacity to conduct advanced phylogeographical analyses of virus sequence data. Additionally, the data generated is potentially useful for disease control and prevention strategies in Kenya and throughout the African continent.

The research questions that this project is addressing are as follows:

1. Are the A(H1N1)pdm09 virus and A(H3N2) virus epidemic patterns in the local community in Kilifi, countrywide in Kenya, and continentwide in Africa a result of multiple introductions of genetically distinct viruses or a single successful introduction event?
2. What are the patterns of spread of A(H1N1)pdm09 and A(H3N2) viruses following community, countrywide, and continentwide introductions, and is there co-circulation of multiple viral lineages?
3. Have viral lineages persisted or faded-out between epidemics over the study period?
4. Was there dominance of a single viral lineage during multiple epidemic seasons?
5. What is the role of the African continent in the global circulation dynamics of influenza viruses?

Vaccination is the major public health measure for the prevention of influenza virus infection and

severe outcomes caused by influenza infections (World Health Organization, 2021). Safe influenza vaccines exist (World Health Organization, 2018a), but effectiveness depends on host immune responses and how well the vaccine strains match the strains in circulation (Osterholm et al., 2012). The WHO convenes technical consultations in February and September each year to recommend virus strains for inclusion in seasonal influenza vaccines for the northern and southern hemispheres, respectively (World Health Organization, 2021). The recommendations are based on information provided by the WHO's Global Influenza Surveillance and Response System (GISRS), which conducts global surveillance of influenza and collects information regarding the circulating seasonal influenza viruses (World Health Organization, 2020a). Most recently, there are efforts to use the phylogenetic patterns of influenza viruses to predict which virus variants will dominate in the future, and therefore should be incorporated into future vaccines using online tools that are able to depict viral evolution in real time (Hadfield et al., 2018).

Since the effectiveness of influenza vaccination depends on knowledge of the diversity of circulating seasonal influenza viruses to guide selection of strains for vaccine formulation, understanding the origins, circulation patterns, viral persistence or fade-out, and viral dominance across geographically defined regions (local community, countrywide, across the continent, and globally) is useful in selecting the most effective vaccine strain for the circulating seasonal influenza viruses. Unfortunately, there is limited information on the diversity of influenza viruses circulating in local communities in Kenya, countrywide in Kenya, and throughout the African continent to contribute to the vaccine strain selection process.

1.14 Hypothesis

Whole-genome sequencing of IAV from a range of sources and times in Kenya and the continent will further understanding of the diversity, evolution, and pathways of spread of these viruses.

1.15 Study Objective

The overall objective is to characterize the sequence diversity, evolutionary dynamics, and patterns of spread of influenza A(H1N1)pdm09 and A(H3N2) viruses in Kenya and across the African continent through WGS data analysis in order to develop an improved understanding of the virus diversity and patterns of spread of A(H1N1)pdm09 and A(H3N2) viruses at various scales of observation (local community, countrywide, continentwide, and worldwide).

1.15.1 Specific Objectives

1. Describe the diversity of influenza A(H1N1)pdm09 and A(H3N2) viruses in the local community in Kilifi, Kenya, countrywide in Kenya, and throughout the African continent. The aims of the objective were to describe the diversity of influenza viruses based on genetic group classification, infer introductions into the local community, the country, and the continent, and reveal the global sources of these introductions.
2. Determine the spatiotemporal patterns of occurrence of influenza A(H1N1)pdm09 and A(H3N2) viruses in the local community in Kilifi, Kenya, countrywide in Kenya, and throughout the African continent. The goal was to establish the spatiotemporal patterns of spread of influenza A(H1N1)pdm09 and A(H3N2) viruses in the local community, countrywide, and in the continent and relate the patterns of spread to the global migration dynamics of influenza viruses using contemporaneous spatiotemporal sequence data from other global regions.
3. Describe the interconnectedness of A(H1N1)pdm09 virus and A(H3N2) virus epidemics at the local community level in Kilifi, countrywide in Kenya, and throughout the African continent. This aimed to elucidate whether different locations in the local community, countrywide, and throughout the continent experience independent introductions of

influenza viruses and if there was spread from one locality to another in the community, countrywide in Kenya, and throughout the continent thus define the pathways of spread of influenza viruses in the community, countrywide, and across Africa.

1.16 Manuscripts the Candidate Contributed to During his PhD Study Period

Here, I list the papers that have either been published or in preparation and are part of the PhD project, and papers that I contributed to while undertaking the PhD that are relevant to my field of research.

1.16.1 Published and Part of the Thesis

1. **Owuor DC**, Ngoi JM, Otieno JR, Otieno GP, Nyasimi FM, Nyiro JU, Agoti CN, Chaves SS, Nokes DJ. Genetic characterization of influenza A(H3N2) viruses circulating in coastal Kenya, 2009-2017. *Influenza Other Respir Viruses*. 2020 May;14(3):320-330. https://doi.org/10.1111/irv.12717.

1.16.2 In Preparation and Part of the Thesis

1. **Owuor DC**, Ngoi JM, Agoti CN, Chaves SS, Nokes DJ (2021). Local patterns of influenza A(H3N2) virus spread in Kilifi, coastal Kenya over a single epidemic season revealed through phylogeographical analyses of virus sequence data (In Preparation).
2. **Owuor DC**, de Laurent ZR, Otieno JR, Kikwai GK, Mayieka LM, Ochieng MO, Otieno NA, Emukule GO, Hunsperger EN, Chaves SS, Nokes DJ, Agoti CN (2021). Phylogeography of influenza A(H1N1)pdm09 virus in Kenya, 2009-2018 (In Preparation).
3. **Owuor DC**, de Laurent ZR, Agoti CN, Chaves SS, Nokes DJ (2021). The role of Africa in the global spread of influenza A(H1N1)pdm09 and A(H3N2) viruses (In Preparation).

1.16.3 Subsidiary but Relevant and Contributed to While Doing the PhD

1. Nyasimi FM, **Owuor DC**, Ngoi JM, Mwihuri AG, Otieno GO, Otieno JR, Githinji G, Nyiro JU, Nokes DJ, Agoti CN. Epidemiological and evolutionary dynamics of influenza B virus in coastal Kenya as revealed by genomic analysis of strains sampled over a single season. *Virus Evolution*. 2020. veaa045, https://doi.org/10.1093/ve/veaa045.
2. Nabakooza G, **Owuor DC**, Zaydah R. de Laurent, Owor N, Kayiwa JT, Jingo D, Agoti CN, Nokes DJ, Kateete DP, Kitayimbwa J, Frost SDW, Lutwama J (2021). Feasibility of influenza whole genome sequencing in Africa: Genomes reveal a nine-year genetic diversity and transmission patterns of influenza in Uganda – In Preparation.

CHAPTER TWO

2 Materials and Methods

2.1 Introduction

This chapter describes the study locations and populations from which samples were collected, the laboratory techniques used to obtain virus sequences, and the methods used to analyze these and other virus sequences from the global dataset. It also includes details of the ethical approvals gained for use of the samples in this project. For improved readability, some of the methods are described within the subsequent chapters as they are specific to those chapters. The study took advantage of a number of sample sets from Kenya and across Africa, residues of which were archived to enable future studies that were not the original intention. This required considerable effort to secure the samples for the new use and also required submission of new requests for ethical approval. This study demonstrates the value of retaining samples in biobanks to be used in the future when new questions are asked and novel techniques to answer new questions are developed.

2.2 Clinical Specimens

Respiratory samples and clinical data related to the processed specimens were extracted from existing study platforms according to the respective case definitions used in these sites. In all the study sites described below, either nasopharyngeal (NP) or oropharyngeal (OP) swabs alone or combined NP/OP swabs were collected. NP swabs were collected from nostrils of patients using polyester-tipped flexible aluminum-shafted swabs (Kim et al., 2011) or nylon-flocked plastic-shafted swabs (Feikin et al., 2017; Hammitt et al., 2011; Nyiro et al., 2018); the swab was inserted into the posterior nasopharynx via the nostril, rotated 180 degrees (Feikin et al., 2017; Kim et al.,

2011) or rotated 2 to 3 times (Hammitt et al., 2011; Nyiro et al., 2018), withdrawn, swab applicator cut-off, and each absorbent swab placed into cryovials containing viral transport medium (VTM) (Feikin et al., 2017; Hammitt et al., 2011; Katz et al., 2014; Kim et al., 2011). For OP swabs, a nylon-flocked plastic-shafted applicator (Kim et al., 2011) or a polyurethane foam-tipped swab (Hammitt et al., 2011) was used to sample the tonsils and posterior oropharyngeal mucosal membrane or Rayon swabs were used to sample over tonsillar pillars and the posterior oropharynx for several seconds (Feikin et al., 2017); swab applicators were cut-off, and each absorbent swab placed into cryovials with VTM (Feikin et al., 2017; Hammitt et al., 2011; Katz et al., 2014; Kim et al., 2011). Specimens were immediately refrigerated or placed in icepacks at 2-8°C, transported to designated laboratories, and stored at −70°C to −80°C until analyzed (Feikin et al., 2017; Hammitt et al., 2011; Kim et al., 2011).

A summary of all the sets of archived samples in the different studies, participating institutions involved, sample sources and types, case definitions for the participating populations, years of surveillance and total samples collected is shown in *Table 2.1*.

Table 2.1: Description of studies, institutions and sample characteristics for IAV positive specimens used in this study.

Study	Participating institutions	Sample sources	Case definition	Sample type(s)	Surveillance years	Number of samples
National Influenza Sentinel Surveillance Study	KEMRI, CDC; Kenya	Inpatient	SARI[a]	NP/OP swabs	2009-2018	41,685
Studying the Pathways of Respiratory virus Disease transmission (SPReD-Kenya) Study	KEMRI, CDC, KWTRP; Kenya	Inpatient	SARI[a] or pneumonia[b]	NP/OP swabs	2014-2016	21,000
Kilifi County and Referral Hospital (KCH) Study	KWTRP; Kenya	Inpatient	LRTI	NP/OP swabs	2009-2018	6,147
Kilifi Health and Demographic Surveillance (SPReD-KHDSS) Study	KWTRP; Kenya	Outpatient	ARI[c]	NP swabs	2015-2017	6,254
Pneumonia Etiology Research for Child Health (PERCH-Africa) Study	PERCH Study Sites; Africa[d]	Inpatient and outpatient	SARI	NP/OP swabs	2011-2013	9,351

[a] Severe acute respiratory illness (SARI) in adult and pediatric wards; [b] Severe pneumonia (including very severe pneumonia, in children aged ≤60 months); [c] Acute respiratory infection (ARI) in all outpatient ages; [d] PERCH-Africa Study sites: KWTRP, Kenya; Medical Research Council (MRC), The Gambia; Hospital Gabriel Toure, Mali; University Teaching Hospital, Zambia; Soweto, South Africa.

Abbreviations: KEMRI, Kenya Medical Research Institute; CDC, Centers for Disease Control and Prevention, Kenya Country office; KWTRP, KEMRI-Wellcome Trust Research Programme; LRTI, lower respiratory tract infection; NP/OP, nasopharyngeal and oropharyngeal.

2.3 Study Designs and Populations

The samples analyzed for this PhD project were from 5 studies described below.

2.3.1 National Influenza Sentinel Surveillance Study (2009-2018)

The Kenyan Ministry of Health in partnership with KEMRI and CDC-Kenya, conducts surveillance for influenza through identification and testing of patients with ILI at outpatient clinics, and patients hospitalized with SARI (Emukule et al., 2014; Emukule et al., 2019; Katz et al., 2014). For this study, only samples from inpatients meeting the SARI case definition were used, which is the focus of this description. SARI was defined as an acute onset of illness (within the last 14 days) among patients who were hospitalized with cough and reported fever or a recorded temperature ≥38°C. Patients meeting the various case definitions, depending on surveillance site, had a structured questionnaire administered by the surveillance officer on site to collect information on signs and symptoms, demographics, and underlying diseases; patients were also assessed by the study clinicians on physical and clinical findings. For hospitalized patients, chart review was also conducted at discharge or death to collect clinical outcome data (Emukule et al., 2019).

Influenza surveillance functions across Kenya and includes sentinel regional hospitals and health facilities at demographic surveillance sites, which represent a variety of demographic characteristics: urban, rural, high mobility, and low socio-economic communities (Emukule et al., 2014; Emukule et al., 2019; Katz et al., 2014; Odhiambo et al., 2012). The hospital sentinel surveillance was set up by the Ministry of Health, Kenya with technical support from CDC-Kenya as a National Influenza Surveillance System in response to the 2005 influenza A(H5N1) virus threat in 2006 and has been in operation since then (Katz et al., 2014). The aims of the surveillance system were to identify circulating influenza virus strains, describe the epidemiology and burden

of influenza in Kenya, and serve as a component of an early warning system for pandemic influenza (Katz et al., 2014). Influenza viruses are typed and subtyped, and the isolates are shared with the WHO reference centers and the USA CDC in Atlanta, Georgia. Aliquots of swab specimens are kept at the local KEMRI laboratory in Kenya and have not been fully utilized to characterize the influenza viruses, for example, characterization of influenza phylogeography in Kenya.

SARI surveillance is conducted in several sites including 1 tertiary referral hospital (KNH), 4 county and referral hospitals (Kakamega, Nakuru, Nyeri, and Siaya), and 1 general teaching and referral hospital (Coast General Teaching and Referral Hospital); *Figure 2.1*. SARI surveillance in Embu and Garissa county and referral hospitals were terminated in 2013 (Breiman et al., 2015; Feikin et al., 2011; Katz et al., 2014).

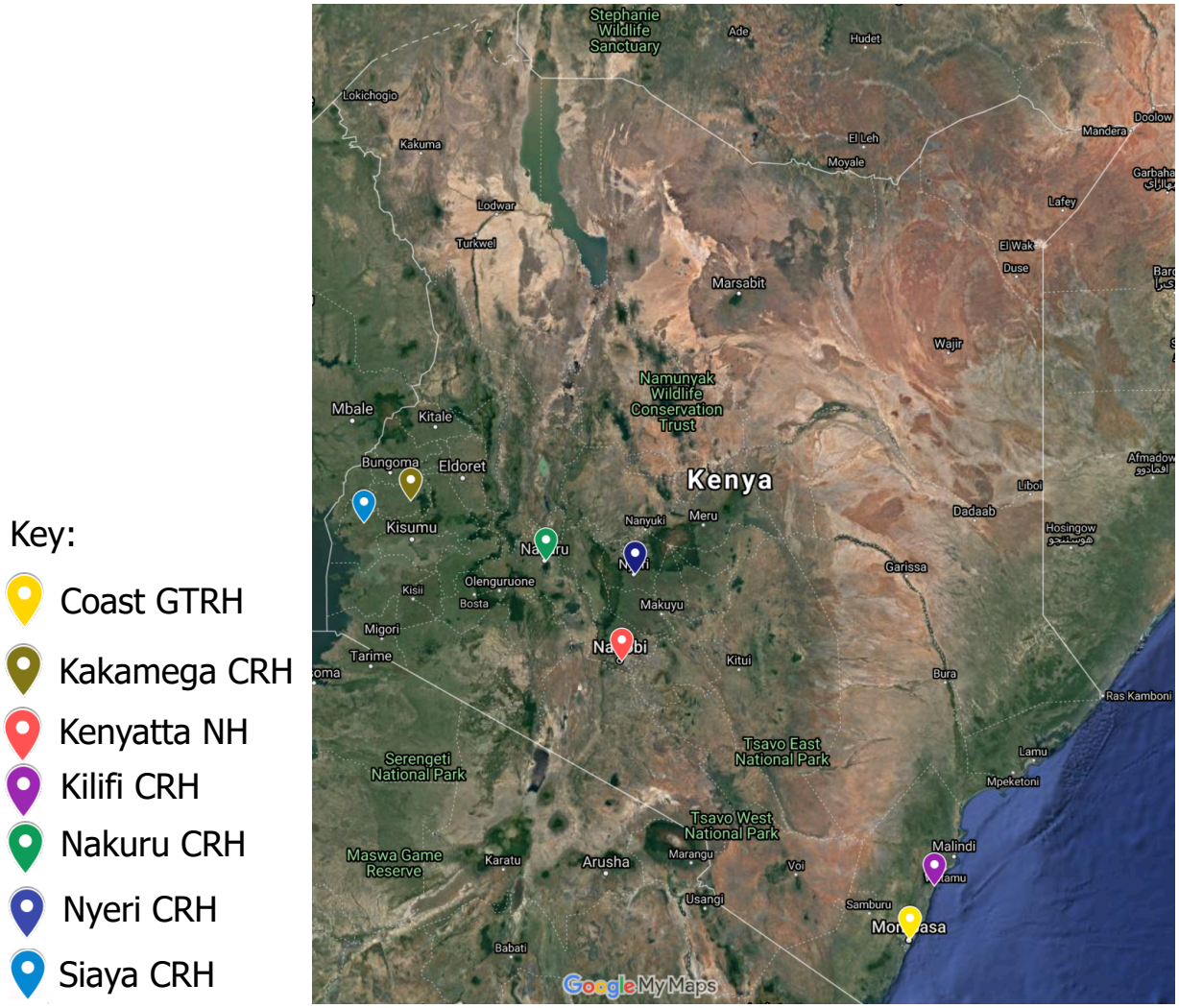


Figure 2.1: Map of Kenya showing the influenza sentinel surveillance sites for SARI used in this study. SARI, Severe Acute Respiratory Illness; GTRH, General Teaching and Referral Hospital; CRH, County and Referral Hospital; NH, National Hospital.

The patient recruitment and specimen collection methods have been described previously (Katz et al., 2014). Briefly, trained surveillance officers (either a nurse or a clinical officer) were employed at each of the surveillance sites; they identified patients at each site who were admitted with respiratory illness on the same day (or the day before) and assessed their eligibility for inclusion in the surveillance platform. Officers identified SARI patients in adult and paediatric inpatient wards in the hospitals from Monday to Friday whereas patients admitted on Saturday were enrolled on Monday if eligibility was met. From August 2006 through December 2011, for each consented individual with SARI at each site, a two-page questionnaire was administered to collect the following information: demographics, underlying diseases, influenza vaccination history, signs and symptoms, and exposures, then NP/OP swabs were collected. Beginning 2008, in-hospital follow-up for SARI patients was conducted to determine final outcome (discharge or death); deaths that occurred within 30 days of hospital admission were considered to be associated with SARI (Katz et al., 2014). For each patient, NP/OP swabs were collected and placed into a single cryovial with VTM, which had been prepared using a standard WHO protocol (World Health Organization, 2006) at KEMRI/CDC-Kenya laboratory in Nairobi and routinely distributed to each of the sentinel surveillance sites (Kim et al., 2011). Specimens were immediately refrigerated at 2-8°C, triple packaged, transported to the NIC in Nairobi or KEMRI/ CDC-Kenya, and stored at −80°C.

The current study utilized archived influenza A(H1N1)pdm09 virus samples collected between 2009 (year of A(H1N1)pdm09 virus emergence) and 2018 to investigate the sequence diversity, evolution, and transmission of A(H1N1)pdm09 virus in Kenya, *Figure 2.1*. These samples were collected as previously described, typed and subtyped for IAV and A(H1N1)pdm09 virus, respectively using real-time reverse transcription polymerase chain reaction (rRT-PCR) at KEMRI/CDC-Kenya laboratory. A total of 41,685 NP/OP swab samples were collected from

admissions of all ages from June 2009 through December 2018 (*Figure 1.5* and *Table 2.1*). Of these, 41,102 swabs were typed for IAV and subsequently subtyped for A(H1N1)pdm09 virus using rRT-PCR employing AgPath kit (Applied Biosystems) (Emukule et al., 2014; Katz et al., 2012a; Katz et al., 2014). A total of 1,307 A(H1N1)pdm09 virus positive samples were obtained. Of these, 418 A(H1N1)pdm09 virus positive samples were available for this project, which were selected based on rRT-PCR Ct (<35.0 with high viral load), adequate sample volume for RNA extraction (>140 µL), and adequate representation of the surveillance sites and years.

2.3.2 Kilifi County and Referral Hospital (KCH) Study (Inpatient Study) (2009-2018)

This study is a long-term inpatient surveillance of respiratory viruses within the Kilifi County and Referral Hospital (KCH) in Kilifi County, Kenya (*Figure 2.1*), which commenced in January 2002 to present (Nokes et al., 2009). The original study objectives were specific to respiratory syncytial virus (RSV), which aimed to quantify the burden of disease requiring hospitalization, define epidemiological patterns, and support immunological and molecular epidemiological investigations within this developing country setting (Nokes et al., 2009; Sande et al., 2013; Scott et al., 2004). Additional viral pathogens including influenza virus (Onyango et al., 2012a), human metapneumovirus (HMPV) (Owor et al., 2016), rhinovirus (HRV) (Onyango et al., 2012b), and coronavirus (HCoV) (Kiyuka et al., 2018), were subsequently included in the surveillance from 2007.

Samples are collected from childhood admissions under the age of 5 years with syndromic severe and very severe pneumonia (using a modified WHO definition) collected as part of continuous viral pneumonia surveillance at KCH (Nokes et al., 2009). Written informed consent was obtained from the parent or guardian of each participant. NP and more recently (from 2010) paired NP and OP samples were collected from each child on the day of admission. The samples analyzed in this

thesis project were collected between January 2009 and December 2018. During this period, a total of 6,147 NP/OP samples were collected from eligible children at KCH (*Table 2.1*). Samples were stored in VTM at −80°C prior to molecular screening and subsequent processing (Nokes et al., 2009; Onyango et al., 2012a). Samples were screened for a range of respiratory viruses, including IAV, using a multiplex (MPX) reverse transcription (RT)-PCR (MPX RT-PCR) assay employing Qiagen QuantiFast RT-PCR kit (Qiagen) (Hammitt et al., 2011). A rRT-PCR Ct of <35.0 was used to define virus-positive samples (Hammitt et al., 2011). A total of 157 IAV positive specimens were identified from KCH; however, these were not subsequently subtyped for influenza A(H1N1)pdm09 virus and A(H3N2) virus subtypes, respectively (Hammitt et al., 2011; Onyango et al., 2012a). Therefore, all 157 IAV positive samples were utilized for this project, *Figure 2.2*.

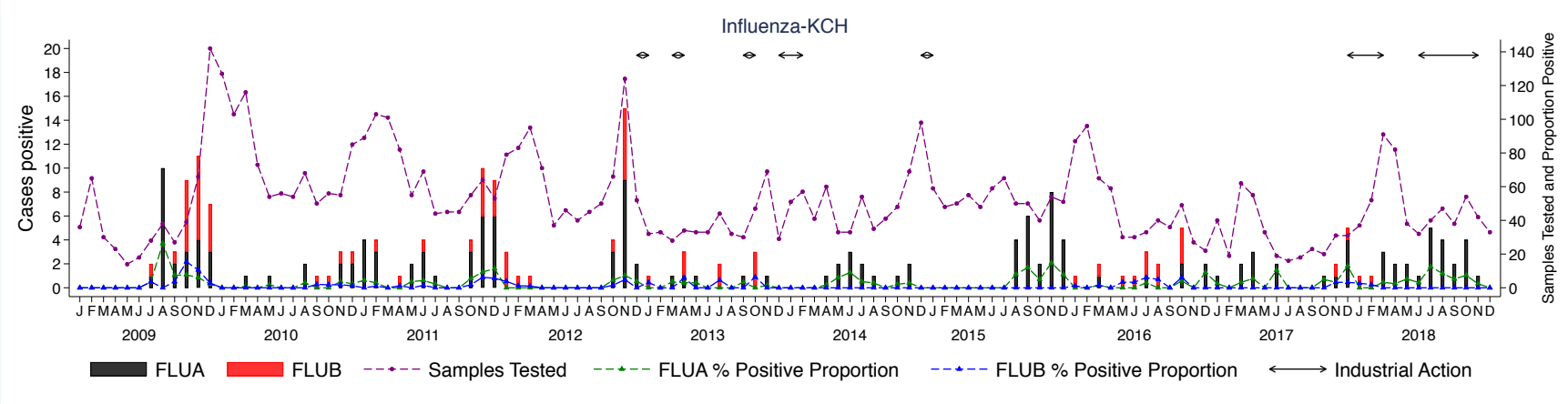


Figure 2.2: Temporal patterns of influenza A and B viruses from KCH, January 2009 to December 2018 (primary Y axis). The dashed line (secondary Y axis) shows the number of samples tested while the topmost solid black lines show periods in which there were healthcare workers' strikes (industrial action) at KCH. FLUA, influenza A virus; FLUB, influenza B virus; KCH, Kilifi County and Referral Hospital.

2.3.3 Studying the Pathways of Respiratory virus Disease transmission (SPReD-Kenya) Study (2014-2016)

The SPReD-Kenya study (http://virec-group.org/spred-kenya/) is part of a larger SPReD study that aimed to advance the understanding of the nature of spread (i.e. characteristic routes of virus introduction, spread, persistence and fade-out) of respiratory viruses (including influenza virus) at different spatial and temporal scales of observation: from the individual to the household and school, and from the local community to the countrywide level, and across the continent. The information obtained from the study will also be useful for innovating public health interventions. The study aimed to integrate epidemiological, virus sequence, contact and mobility data at the different scales of observation.

The SPReD-Kenya study is a collaborative project between KWTRP and KEMRI/CDC-Kenya, which aimed to collect and analyze approximately 7,000 respiratory specimens per year between 2014 and 2016 from 10 sentinel surveillance sites across Kenya from patients of all ages with SARI or ILI. Seven of the 10 SARI sites, which provided specimens for this study were: KNH, Coast General Teaching and Referral Hospital, Kakamega County and Referral Hospital, Nyeri County and Referral Hospital, Siaya County and Referral Hospital, Nakuru County and Referral Hospital, and Kilifi County and Referral Hospital; *Figure 2.1*.

2.3.4 Kilifi Health and Demographic Surveillance System (SPReD-KHDSS) Study (2015-2017)

The SPReD-KHDSS study (Nyiro et al., 2018) (http://virec-group.org/local-spred/) is also part of the larger SPReD study, which specifically focusses on the KHDSS. It also aims to map the patterns of spread of influenza viruses (Nyasimi et al., 2020; Owuor et al., 2020) and other respiratory viruses using epidemiological and virus sequence data. For this study, samples were

collected between December 2015 and March 2017 from patients of all ages presenting to 9 selected outpatient health facilities within the KHDSS with one or more ARI symptoms as defined by the WHO. The selected 9 outpatient health facilities were: Chasimba, Jaribuni, Junju, Matsangoni, Mavueni, Mtondia, Ngerenya, Pingilikani, and Sokoke, whose selection was based on representation across the KHDSS, coverage of major road networks, and variation in population density (Nyiro et al., 2018) (*Figure 2.3*).

The patient recruitment and specimen collection methods have been descried previously (Nyiro et al., 2018). Briefly, the recruitment of patients into the study and collection of specimens were integrated within the routine patient care at the 9 selected outpatient health facilities, which was led by a resident clinician or study nurse. Each facility had 1 or 2 sampling days per week between Monday and Friday (09:00 A.M. to 01:00 P.M.). On each sampling day, a study fieldworker stationed at the health facility assisted by the resident clinician or nurse, described the study to the attending patients. Any person presenting with signs and symptoms of ARI was asked to see the fieldworker for further screening and to be consented while they awaited review by the study clinician or nurse. Patients of all ages presenting with one or more symptoms of cough, difficulty breathing, sneezing, nasal congestion, or increased respiratory rate for age (as defined by the WHO) were eligible. However, newborns aged <7 days and patients with ARI for more than 30 days were excluded from the study. Written informed consent was sought from adult patients and parents/guardians of patients <18 years then samples were collected. A target of 15 samples per week was utilized on a 'first-come, first-served' basis as they presented to the health facilities on the set sampling days between December 2015 and March 2017 (*Figure 2.4*). The sample size of 15 samples per site per week was determined based on outpatient data on the number of respiratory

infection cases per month per selected health facility. A standard questionnaire was administered to collect biodata, presenting symptoms and treatment received (Nyiro et al., 2018).

A total of 6,254 NP swab samples were collected from outpatients of all ages presenting with ARI to selected 9 outpatient health facilities spread throughout the KHDSS between December 2015 and March 2017 (*Table 2.1*). These were stored in cryovials containing VTM, kept at 8°C in an ice-packed cool box for return to KWTRP within 4 hours of collection, and stored at −80°C prior to molecular screening and subsequent processing (Hammitt et al., 2011; Nyiro et al., 2018). Samples were screened for a range of respiratory viruses, including IAV, using a MPX rRT-PCR assay employing Qiagen QuantiFast RT-PCR kit (Qiagen) (Hammitt et al., 2011). A rRT-PCR Ct of <35.0 was used to define virus-positive samples (Hammitt et al., 2011). A total of 96 IAV positive specimens were identified from the KHDSS. However, these were not subsequently subtyped for influenza A(H1N1)pdm09 virus and A(H3N2) virus subtypes, respectively (Nyiro et al., 2018). Therefore, all 96 IAV samples were utilized for this project; *Figure 2.4*.

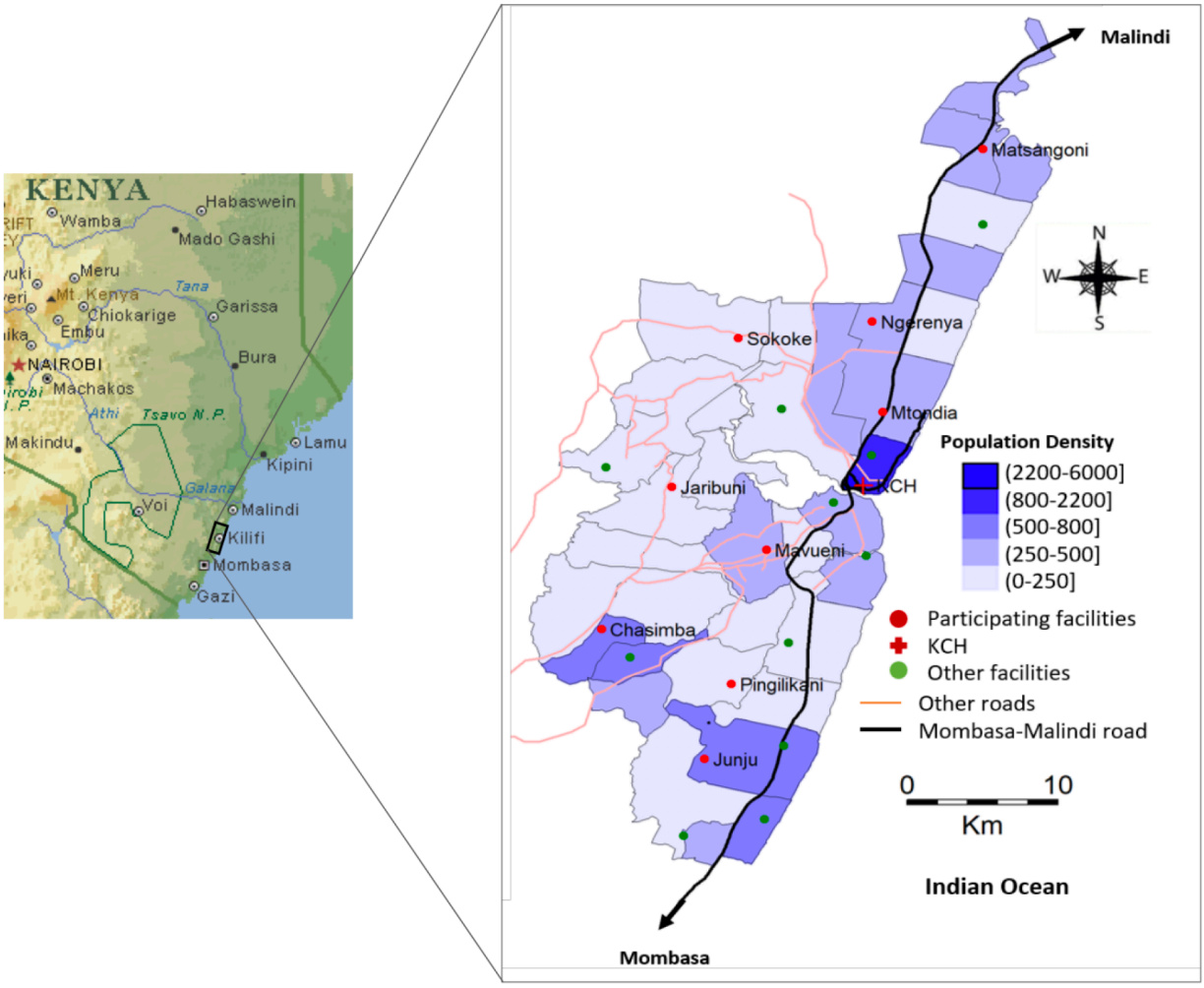


Figure 2.3: A map of the SPReD-KHDSS study sites adopted from (Nyiro et al., 2018). The map showing the KHDSS is expanded from the map of Kenya. It shows the population density (person per Km^2) and the 9 selected outpatient health facilities (red circles) where the study was conducted. The green markers show the other public health facilities within the KHDSS. KCH is also shown. KCH, Kilifi County and Referral Hospital.

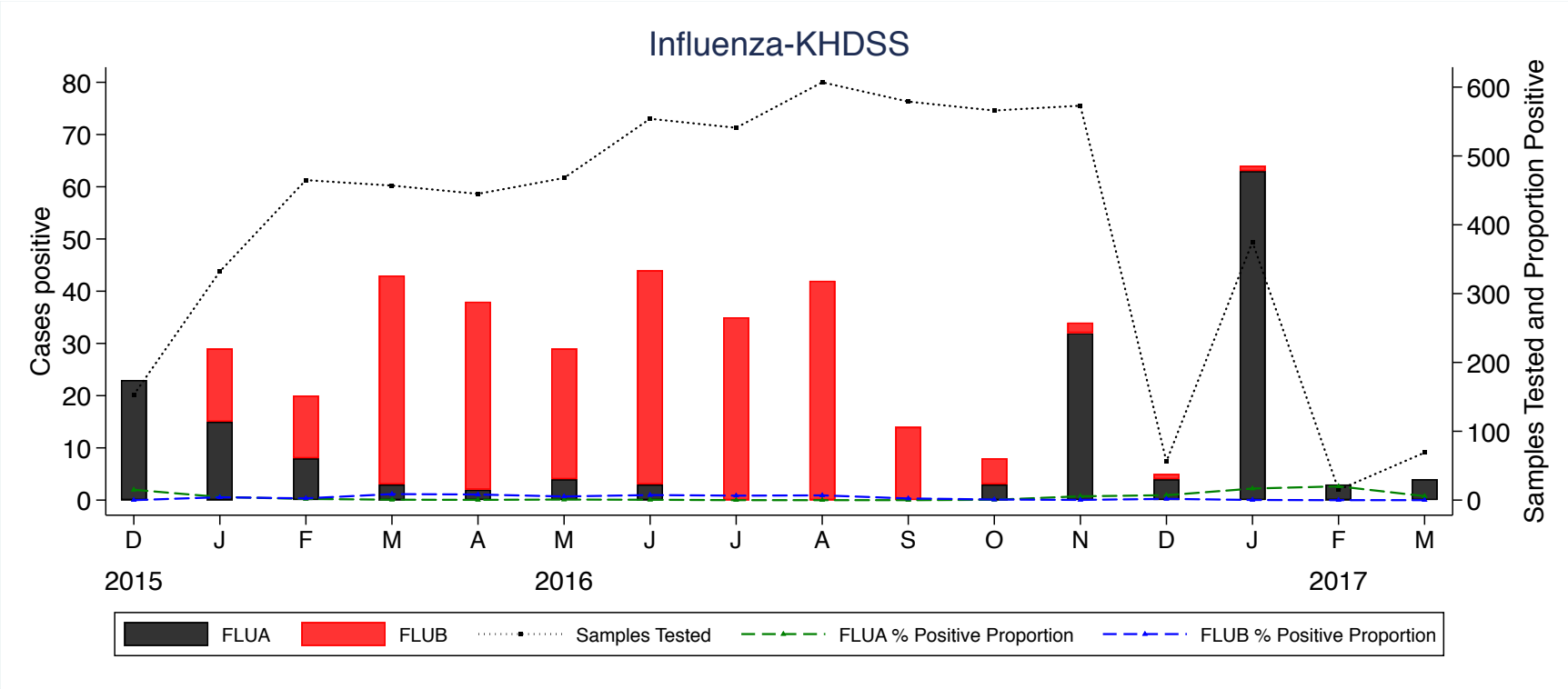


Figure 2.4: Temporal patterns of influenza A and B viruses from the SPReD-KHDSS study, 2015-2017 (primary Y axis). The black dashed line (secondary Y axis) shows the number of samples tested. FLUA, influenza A virus; FLUB, influenza B virus; KHDSS, Kilifi Health and Demographic Surveillance Study.

2.3.5 Pneumonia Etiology Research for Child Health (PERCH-Africa) Study (2011-2013)

The PERCH project was a multi-country, standardized, comprehensive case-control study of severe or very severe pneumonia carried out in 9 sites in 7 participating countries (Deloria-Knoll et al., 2012; Levine et al., 2012; Scott et al., 2012b). The study was carried out in 9 sites in 5 African countries (Basse, The Gambia; Bamako, Mali; Kilifi, Kenya; Soweto, South Africa; and Lusaka, Zambia) (*Figure 2.5*) and 2 Asian countries (Dhaka and Matlab, Bangladesh; and Nakhon Phanom and Sa Kaeo, Thailand), that represent 2 geographic regions where the vast majority of the world's severe and fatal pneumonia cases occur, and which represent a range of socioeconomic backgrounds, urban and rural environments, variations in HIV infection and malaria prevalence, and different altitudes (Deloria-Knoll et al., 2012; Levine et al., 2012; O'Brien et al., 2019). In Africa, the studies were led by the following institutions: Medical Research Council (MRC) in The Gambia; KWTRP in Kenya; Hospital Gabriel Toure in Mali; and the University Teaching Hospital in Zambia (Levine et al., 2012; O'Brien et al., 2019). The study aimed to evaluate the etiological agents causing severe or very severe childhood pneumonia in developing countries in the pneumococcal and *Haemophilus influenzae* tybe b conjugate vaccine era and is the largest study of its kind since the 1980s and since the development of modern molecular diagnostics (Levine et al., 2012; Selwyn and Researchers, 1990). Cases were children aged 1-59 months admitted to hospital with WHO-defined severe and very severe pneumonia (pre-2013 definition) (World Health Organization, 2005) whereas controls were age-group, time, and location matched children without pneumonia randomly selected from communities surrounding the study sites (Deloria-Knoll et al., 2012; Levine et al., 2012; O'Brien et al., 2019). The use of hospitalized patients was necessary to ensure safe collection of a range of specimens from patients and to allow for efficiency

of testing only for those with severe or very severe pneumonia. On the other hand, the inclusion of controls was important to guide the interpretation of results from the use of highly sensitive detection tests on upper respiratory tract specimens and to facilitate the identification of risk factors for pneumonia and/or specific etiologies (Levine et al., 2012).

The study aimed to recruit ~6,000 patients hospitalized for severe or very severe pneumonia and ~6,000 controls randomly from the community; each site recruited participants for 2 years between August 2011 and January 2014 (Deloria-Knoll et al., 2012; Levine et al., 2012). Case enrolment, specimen collection and laboratory procedures were standardized (Crawley et al., 2017; Deloria-Knoll et al., 2012; Murdoch et al., 2012; Scott et al., 2012b). At all the sites, clinical assessment and enrolment of PERCH cases and controls were conducted by clinicians (i.e. doctors, nurses, and clinical officers). Nurses and field workers or research assistants took anthropometric measurements, assisted clinicians with the procedures, and identified and located PERCH community controls in all sites (Crawley et al., 2017). The PERCH case definition was based on the 2005 WHO clinical definition of severe or very severe pneumonia (Scott et al., 2012b) with enrolment period predating the 2013 reclassification of severe or very severe pneumonia by the WHO (World Health Organization, 2013).

Cases were enrolled at the time of presentation to the hospital. Severe pneumonia was defined as cough or difficulty in breathing with lower chest wall indrawing, whereas very severe pneumonia was defined as cough or difficulty in breathing and at least one of the following signs: difficulty in breastfeeding or drinking, vomiting everything, central cyanosis, convulsions, lethargy, unconsciousness, or head nodding (O'Brien et al., 2019; World Health Organization, 2013). However, elevated respiratory rate was not part of the case definitions. The exclusion criteria for cases and controls were hospitalization within the preceding 14 days, having been discharged as a

PERCH case within the past 30 days, and residence outside the study catchment area. An additional exclusion criterion for cases was resolution of lower chest wall indrawing after bronchodilator therapy for children with wheeze (Deloria-Knoll et al., 2012; O'Brien et al., 2019). At all sites, case assessment occurred within 24 hours of admission with each site enrolling participants over a 24-month period. Case screening was done 24 hours per day and 7 days per week at KWTRP during which all eligible consenting cases were enrolled. At the remaining sites, screening was done during established hours whereby all eligible consenting cases presenting during predefined screening hours were enrolled except for Mali, which used a systematic sampling process. Controls were randomly selected from residents of the same catchment area as cases and frequency matched to cases by age-group (1 to <6 months, 6 to <12 months, 12 to <24 months, and 24-59 months of age) and were enrolled regardless of respiratory symptoms to provide the least biased comparison for estimating pneumonia causes, but were ineligible if they met the PERCH case definition (Deloria-Knoll et al., 2012; O'Brien et al., 2019). Cases underwent clinical examination at admission, at 24 hours, and at 48 hours (if the child was still hospitalized) including assessments of respiratory signs, anthropometric measurements, and peripheral oxygen saturation (on room air whenever it was possible) (Crawley et al., 2017). The vital status of cases was assessed during follow-up visit or telephone interview done 30 days after admission (with a window of 21-90 days). Controls were similarly assessed for clinical findings at enrolment but had no follow-up assessment (The PERCH Study Group, 2012).

The PERCH-Africa study samples analyzed in this thesis project were collected between August 15, 2011 and January 30, 2014. During this period, 4,232 (73.9%) of 5,723 eligible children with severe or very severe pneumonia and 5,119 (56.9%) of 5,478 eligible community controls within the study catchment areas were enrolled in the 9 study sites in the 7 countries; 3,981 (94.1%) of

4,232 cases and 5,102 (99.7%) of 5,119 controls categorized as without HIV infection were analyzed. At enrolment, NP/OP swabs, lung aspirate, and pleural fluid were collected and tested with multiplex quantitative PCR, culture, or both (Driscoll et al., 2017; O'Brien et al., 2019). Following collection, NP/OP swabs were placed in VTM and processed within 24 hours of collection. Specimens were left in room temperature for no more than 2 hours or at 4°C for no more than 24 hours before freezing at −70°C. All samples were tested in-country using standardized methodology (Driscoll et al., 2017; Feikin et al., 2017; O'Brien et al., 2019). Samples were screened for a range of respiratory pathogens, including IAV, using a Fast-track Diagnostics respiratory Pathogens 33 multiplex kit (FTD Resp-33 kit) (Fast-track Diagnostics) (Feikin et al., 2017; O'Brien et al., 2019). For this thesis project, only IAV positive samples from 5 sites in the 5 African countries were analyzed (*Figure 2.5*). A total of 127 IAV positive specimens were identified from the 5 sites in the 5 African countries. However, these were not subsequently subtyped for influenza A(H1N1)pdm09 virus and A(H3N2) virus subtypes, respectively. Therefore, all 127 IAV positive samples were utilized for this project.

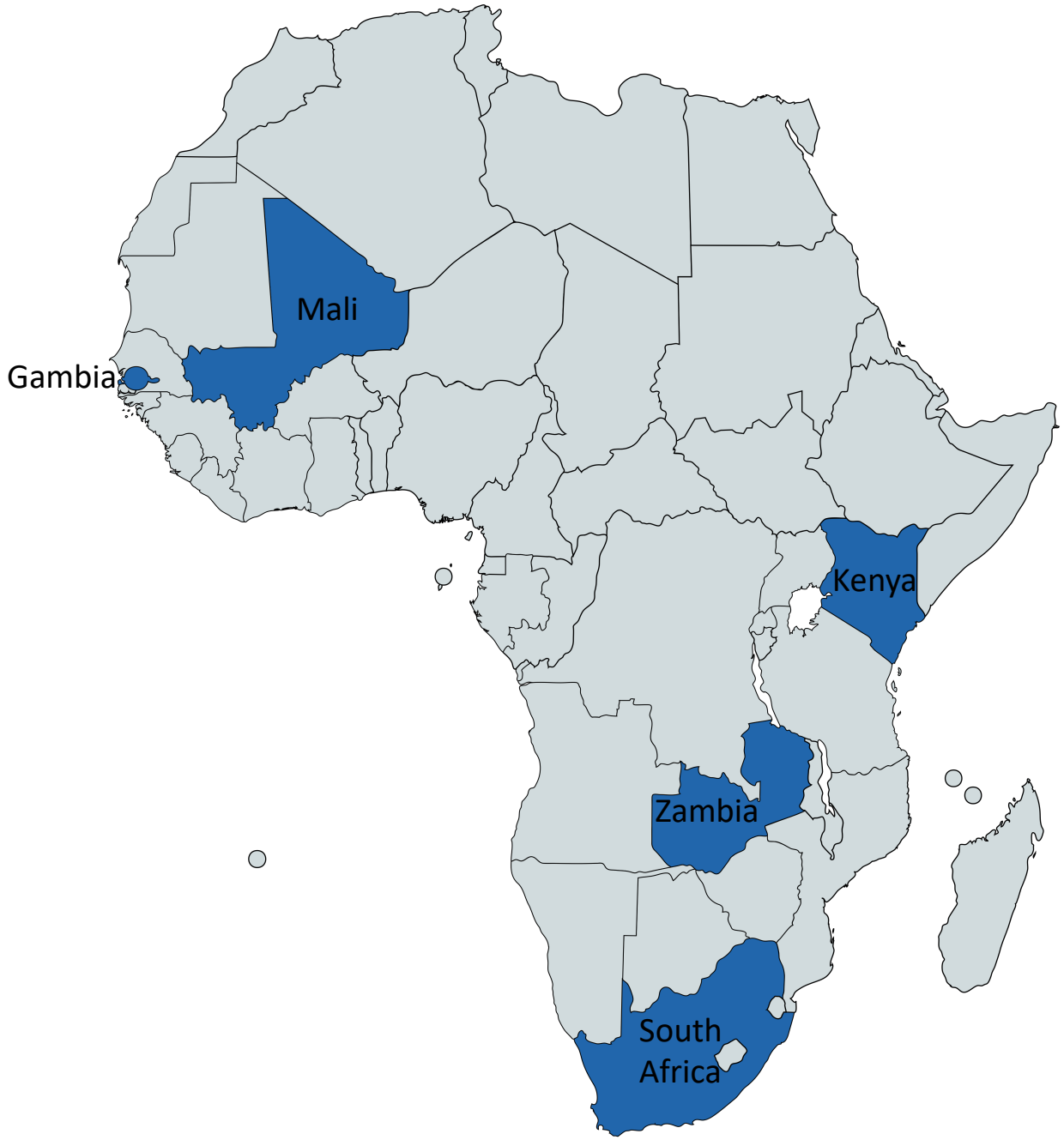


Figure 2.5: PERCH study surveillance sites in Africa, which include The Gambia, Kenya, Mali, South Africa, and Zambia. PERCH, Pneumonia Etiology Research for Child Health.

2.4 Study Scientific and Ethical Approval

The description below focuses first on the collections of samples from Kenya used to explore IAV transmission and evolution within country, and second on samples from across Africa from the PERCH-Africa study looking at inter-country transmission and evolution of IAV. All the source studies had archived samples with ethical approval for future use. Specific approval for the present research was then gained from relevant review boards from Kenya and internationally.

2.4.1 Kenya Samples

Samples used in this study that had previously been collected and stored from the sites in Kenya had received scientific and ethical approval from the UK (Coventry Research Ethics Committee), and Kenyan (KEMRI Scientific and Ethics Review Unit (SERU)) ethics committees, CDC-Kenya/ Ministry of Health National Influenza Sentinel Surveillance Program (Katz et al., 2014) and KWTRP (Nokes et al., 2008), *Table 2.2*. The SPReD-Kenya study was approved by KEMRI SERU while the SPReD-KHDSS study was approved by both the KEMRI SERU and University of Warwick Biomedical and Scientific Research Ethics Committee (Nyiro et al., 2018), *Table 2.2* and *Appendix 7.1*. A written informed consent was obtained from the study patient or their guardian.

2.4.2 Africa Samples

Samples used in this study from the PERCH-Africa study that had previously been collected and stored from the PERCH-Africa sites had received scientific and ethical approval from institutional ethics review boards within each study country in Africa, the UK, and USA (The PERCH Study Group, 2012). Additional ethical approval was sought and received from KEMRI SERU and Oxford Tropical Research Ethics Committee (OxTREC), *Table 2.2* and *Appendix 7.1*. A written informed consent was obtained during case and control enrolment whereas a verbal consent was

obtained during follow-up telephone interviews of cases done 30 days after admission to determine their vital status.

Table 2.2: Summary of scientific and ethics review approvals and type of consent for the use of samples in this study.

Study	SERU	Consent
National Influenza Sentinel Surveillance Study	KEMRI SSC No. 1899, 2558 and 2692	Written
Studying the Pathways of Respiratory virus Disease transmission (SPReD-Kenya) Study	SERU No. 3044	Written
Kilifi County and Referral Hospital (KCH) Study	KWTRP SSC No. 1055 and 1433	Written
Kilifi Health and Demographic Surveillance (SPReD-KHDSS) Study	SERU No. 3103 and BSREC# REGO-2015-6102	Written
Pneumonia Etiology Research for Child Health (PERCH-Africa) Study	SSC No. 1055 and OxTREC Ethics ID:60-90	Written and verbal

Abbreviations: KEMRI, Kenya Medical Research Institute; KWTRP, KEMRI Wellcome Trust Research Programme; SERU, Scientific and Ethics Review Unit; SSC, Scientific and Steering Committee; OxTREC, Oxford Tropical Research Ethics Committee.

2.5 Laboratory Methods

The description below focuses first on the laboratory methods used to amplify and sequence IAV genomes, second on short-read data assembly of the IAV genomes, and third on the collation of global comparison datasets for contextualization of IAV genomes from Kenya and Africa. The collections of samples from Kenya and across Africa were selected from the studies described in section 2.3 (*Table 2.1*), which were selected based on prescreening test results described for each study in each study section. A summary of the studies, study period, and corresponding sample numbers used for the current analyses is shown in *Table 2.3*.

A key goal of my project was to establish WGS of IAV in Kenya, which was part of technology transfer from the USA CDC Influenza Genomics team. The study utilized established techniques by receiving protocols for IAV sequencing from the CDC Advanced Molecular Detection program (https://www.cdc.gov/flu/about/advanced-molecular-detection.htm).

Table 2.3: Description of studies, surveillance years and number of samples used in the study.

Study	Surveillance years	Number of samples
National Influenza Sentinel Surveillance Study	2009-2018	418
Studying the Pathways of Respiratory virus Disease transmission (SPReD-Kenya) Study	2014-2016	
Kilifi County and Referral Hospital (KCH) Study	2009-2018	157
Kilifi Health and Demographic Surveillance (SPReD-KHDSS) Study	2015-2017	96
Pneumonia Etiology Research for Child Health (PERCH-Africa) Study	2011-2013	127

2.5.1 IAV Diagnosis and RNA Extraction from IAV Positive Samples

All respiratory specimens analyzed in this project from all the studies were diagnosed for IAV using rRT-PCR assay employing AgPath kit (Applied Biosystems) (Katz et al., 2014), multiplex rRT-PCR assay employing Qiagen QuantiFast RT-PCR kit (Qiagen) (Hammitt et al., 2011), and rRT-PCR assay employing FTD Resp-33 kit (Fast-track Diagnostics) (O'Brien et al., 2019). Viral nucleic acid extraction from IAV positive samples (Ct <35.0) was performed using the QIAamp Viral RNA Mini Kit (Qiagen). The kit offers rapid isolation of high-quality, ready-to-use RNA

with consistent high yields and complete removal of contaminants and inhibitors; https://www.qiagen.com/us/shop/pcr/qiaamp-viral-rna-mini-kit/.

2.5.2 Multi-Segment Reverse Transcription-Polymerase Chain Reaction (M-RTPCR)

Each IAV RNA segment contains conserved non-coding regions of different lengths at both the 5'- and 3'-ends. The extreme terminal 12 to 13 nucleotides at both the 5'- and 3'-ends of viral RNA segments are highly conserved among all genome segments of IAV, which is followed by a segment-specific non-coding region (Bouvier and Palese, 2008). Most of the techniques used to study the segmented IAV genome begin by purifying RNA from the virus, or infected cells, converting it to complementary DNA, then to double stranded DNA, and amplifying the double stranded DNA using RT-PCR. The RT-PCR amplicons can then be sequenced or cloned into vectors for further analysis. The M-RTPCR technique was developed to simultaneously amplify the 8 genomic RNA segments of IAV in a single reaction irrespective of virus strain, which generates IAV amplicons (Zhou et al., 2009; Zhou and Wentworth, 2012). M-RTPCR takes advantage of the highly conserved 5'- and 3'-ends of IAV genome segments and uses one pair of primers to amplify all the genomic viral RNA segments (Zhou et al., 2009). M-RTPCR is therefore a more efficient method for IAV amplification compared to multiplex RT-PCR strategies that use multiple primer pairs in separate RT-PCR reactions (Deng et al., 2015; Hoper et al., 2011; Rutvisuttinunt et al., 2013). The use of multiple reactions in multiplex RT-PCR is labor intensive and results in long turnaround time for experiments. M-RTPCR amplification of viruses directly from specimens is ideal for high-throughput sequencing and applicable for several DNA array platforms; it also provides sequence information free of artifacts that are often selected during virus propagation (Zhou et al., 2009). The technique has been utilized in WGS studies of IAV by

generating virus amplicons directly from clinical specimens in both clinical and research settings (Goldstein et al., 2017; Meinel et al., 2018; Owuor et al., 2020).

The M-RTPCR technique was adapted from the USA CDC Influenza Genomics team protocols. The goals of the initial laboratory experiments were to optimize the technique. First, due to differences in laboratory machines used at KWTRP from those recommended in the protocol, for example, the Veriti™ PCR machine (Thermo Fisher Scientific) used in KWTRP for IAV amplicon generation instead of the recommended ProFlex™ PCR machine (Thermo Fisher Scientific) and the BioAnalyzer System (Agilent Technologies) for library fragment size analysis instead of the recommended QIAxcel Fragment Analyzer (Qiagen). Second, due to differences in some of the reagents in use at KWTRP from those recommended in the protocol, for example, 2% Agarose gel (Sigma-Aldrich) for visualization of successful amplification of IAV amplicons following M-RTPCR instead of the recommended precast Agarose E-gels (Invitrogen). Extracted RNA was reverse transcribed and the entire IAV genome was amplified in a single M-RTPCR reaction using the Uni/Inf primer set (Zhou and Wentworth, 2012). The amplification was performed in 25 µL reactions containing 8 µL nuclease-free water, 12.5 µL 2× RT-PCR buffer, 0.2 µL Uni12/Inf1 (10 µM), 0.3 µL Uni12/Inf3 (10 µM), 0.5 µL Uni13/Inf1 (10 µM), 0.5 µL SuperScript III One-Step RT-PCR with Platinum *Taq* High Fidelity (Invitrogen) and 3 µL extracted viral RNA as shown in the master mix reaction in *Table 2.4*. Thermocycling conditions were as follows: 42°C for 50 minutes, 50°C for 10 minutes, 94°C for 2 minutes; 4 cycles (94°C for 30 seconds, 43°C for 30 seconds and 68°C for 3 minutes and 50 seconds) followed by 30 cycles of 94°C for 30 seconds, 57°C for 30 seconds, and 68°C for 3 minutes and 30 seconds (with the 3 minutes and 30 seconds for the 68°C extension step increased by 10 seconds per subsequent cycle after cycle 1); and a final extension step at 68°C for 10 minutes. Successful amplification was evaluated by running IAV

amplicons on a 2% Agarose gel (Sigma-Aldrich) and visualized on a UV trans-illuminator after staining with RedSafe Nucleic Acid Staining solution (iNtRON Biotechnology Inc.,); *Figure 2.6*. All successfully amplified amplicons were evaluated for quantity and purity with Quant-iT dsDNA High Sensitivity Assay (Invitrogen) and NanoDrop Spectrophotometer (Thermo Fisher Scientific), respectively. The amplicons with high quantity (> 5 ng/µL) and quality (within a range of 2.0-2.2 at 260/230 nm spectrophotometer absorbance in the NanoDrop) were selected for NGS.

Table 2.4: Preparation of M-RTPCR reaction master mix.

Description	**1 reaction (µL)**
RT-PCR buffer	12.5 µL
SuperScript III *Taq* polymerase	0.5 µL
Uni/Inf primer set mix	1 µL
Nuclease-free water	8 µL
Template RNA	3 µL
Total reaction volume	**25 µL**

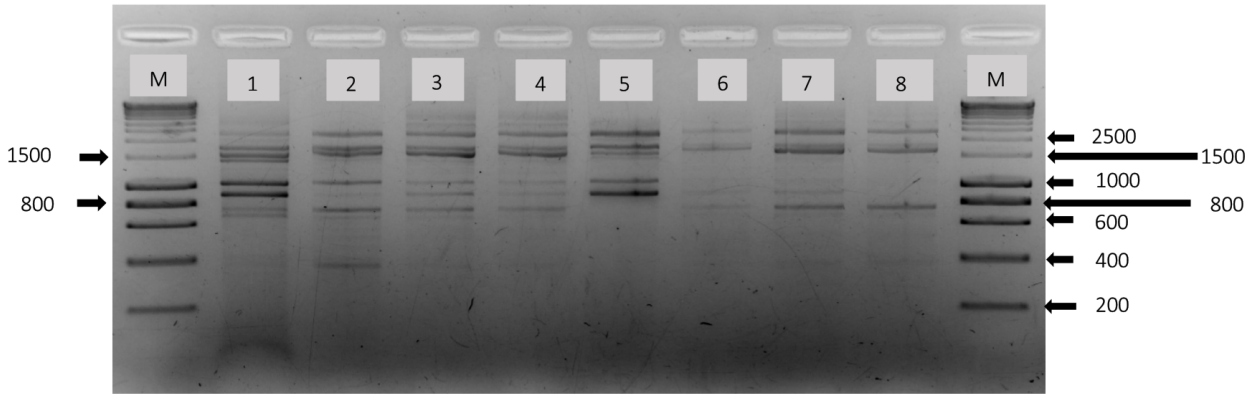


Figure 2.6: Agarose gel electrophoresis image of amplified IAV amplicons using M-RTPCR. The first and last lanes represent the molecular markers for sizing the viral genome segments. Lanes labelled 1 to 8 represent successfully amplified amplicons for 8 individual IAV samples. All the 8 IAV genome RNA segments are resolved in each of the 8 sample lanes as shown (labelled 1-8 in the gel image); the presence of 8 segments in the gel suggests successful amplification of IAV amplicons. The segments are separated in the gel by size; the largest segments are resolved near the amplicon loading wells (wells above the labelled sample wells M-1-8-M) whereas the smallest segments are resolved further along the columns (below the labelled sample wells M-1-8-M). IAV, influenza A virus; M-RTPCR, multi-segment reverse transcription-polymerase chain reaction; M, molecular ladder.

2.5.3 IAV Sequencing through NGS

An overall discussion of IAV NGS using Illumina Nextera XT Sample Preparation Kit (https://www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/nextera-xt-dna.html) and Illumina MiSeq System (https://www.illumina.com/systems/sequencing-platforms/miseq.html) directly from clinical samples was provided in Chapter 1, section 1.12. The advantages of performing NGS using the Nextera XT kit and virus sequencing using the MiSeq System over Sanger sequencing and other NGS technologies were also discussed. The techniques

for IAV library preparation using the Nextera XT kit and subsequent MiSeq sequencing was adapted from protocols provided by the USA CDC Influenza Genomics team, which is the method of choice for IAV sequencing in the CDC laboratory and forms part of CDC Advanced Molecular Detection program (https://www.cdc.gov/flu/about/advanced-molecular-detection.htm). However, several optimization reactions were performed to generate high quality output from library preparation.

Following PCR, the amplicons were purified with 1× AMPure XP beads (Beckman Coulter Inc.,), quantified with Quant-iT dsDNA High Sensitivity Assay (Invitrogen), and normalized to 0.2 ng/μL. Quantification of amplicons was necessary in order to select amplicons with higher concentrations (> 5 ng/μL). Indexed paired-end libraries were generated from 2.5 μL of 0.2 ng/μL amplicon pool using Nextera XT Sample Preparation Kit (Illumina) following the manufacturer's protocol. Amplified libraries were purified using 0.8× AMPure XP beads, quantitated using Quant-iT dsDNA High Sensitivity Assay (Invitrogen), and evaluated for fragment size in the Agilent 2100 BioAnalyzer System using the Agilent High Sensitivity DNA Kit (Agilent Technologies). Libraries were then diluted to 2nM in preparation for pooling and denaturation for running on the Illumina MiSeq (Illumina). Pooled libraries were sodium hydroxide (NaOH) denatured, diluted to 12.5 picomolar and sequenced on the Illumina MiSeq using version 2 (2 × 250 base pair (bp)) and version 3 (2 × 300 bp) paired-end reads with the MiSeq v2 500 and v3 600 cycle kits, respectively (Illumina). The 2 × 250 bp kit is used to sequence 250 bp amplicon fragments while the 2 × 300 is used to sequence 300 bp amplicon fragments, which generates sequencing reads of 250 bp and 300 bp in size, respectively. Five percent Phi-X (Illumina) spike-in was added to the libraries to increase library diversity by creating a more diverse set of library clusters. Low diversity libraries are common for amplicon pools and occurs when a significant number of reads have similar

sequences, for example, in amplicon pools as used in this study. A simplified illustration of the workflow for viral RNA isolation, amplification of IAV amplicons using M-RTPCR, library preparation from IAV amplicons, and sequencing on the MiSeq System is shown in *Figure 2.7*. The initial MiSeq runs were performed to optimize library preparation using IAV amplicons. It was important to define an optimal final library concentration for sequencing (a range of 8 to 15 picomolar was evaluated) and the best version of the library preparation kits for sequencing (both 2 × 250 bp and 2 × 300 bp kits were evaluated). A final library concentration of 12.5 picomolar was selected as the optimal concentration for IAV amplicon sequencing using both the 2 × 250 bp and 2 × 300 bp kits, respectively. The 2 × 250 bp and the 2 × 300 bp kits are 500-cycle and 600-cycle sequencing kits, respectively; the 2 × 300 bp kit allows the longest read length of any Illumina sequencing system (https://www.illumina.com/products/by-type/sequencing-kits/cluster-gen-sequencing-reagents/miseq-reagent-kit-v3.html). A total of 96 IAV amplicon libraries were sequenced per sequencing reaction with the multiplexing of 96 libraries per reaction facilitated by the use of 96 unique indexes from the Nextera XT kit, which allowed indexing of individual amplicons prior to pooling and sequencing (https://www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/nextera-xt-dna.html). Following sequencing, the run output files that were generated during the sequencing reactions in the MiSeq System were analyzed using cloud-based Illumina BaseSpace platform (https://www.illumina.com/products/by-type/informatics-products/basespace-sequence-hub.html) to examine the run metrics and determine successful sequencing reactions. Summaries of the first 4 MiSeq sequencing runs using 2 × 250 bp and 2 × 300 bp library preparation kits are shown in *Figure 2.8* and *Figure 2.9*, respectively. The summaries show sequencing runs used for optimization of library preparation and an optimized library preparation reaction with subsequent sequencing for the 2 × 250 bp and

2 × 300 bp kits, respectively. Optimized library preparation reactions and subsequent MiSeq sequencing yielded: (i) more data (expected output: 2 × 250 bp kit, 7.5-8.5 Gb; 2 × 300 bp kit, 13.2-15 Gb); (ii) more sequencing reads passing quality control filters (expected paired-end yield: 2 × 250 bp, 24-30 million reads; 2 × 300 bp, 44-50 million reads); and (iii) sequencing cluster densities within expected range, which suggest successful sequencing (cluster density range for balanced libraries: 2 × 250 bp kit, 1000-1200 K/mm^2; 2 × 300 bp kit, 1200-1400 K/mm^2) than library preparation of non-optimized runs; *Figure 2.8* and *Figure 2.9*. Based on the run metrics, the 2 × 300 bp kit was the kit of choice for sequencing and was used in 7 of the 10 MiSeq sequencing runs that were performed in order to test all the IAV samples available for this study.

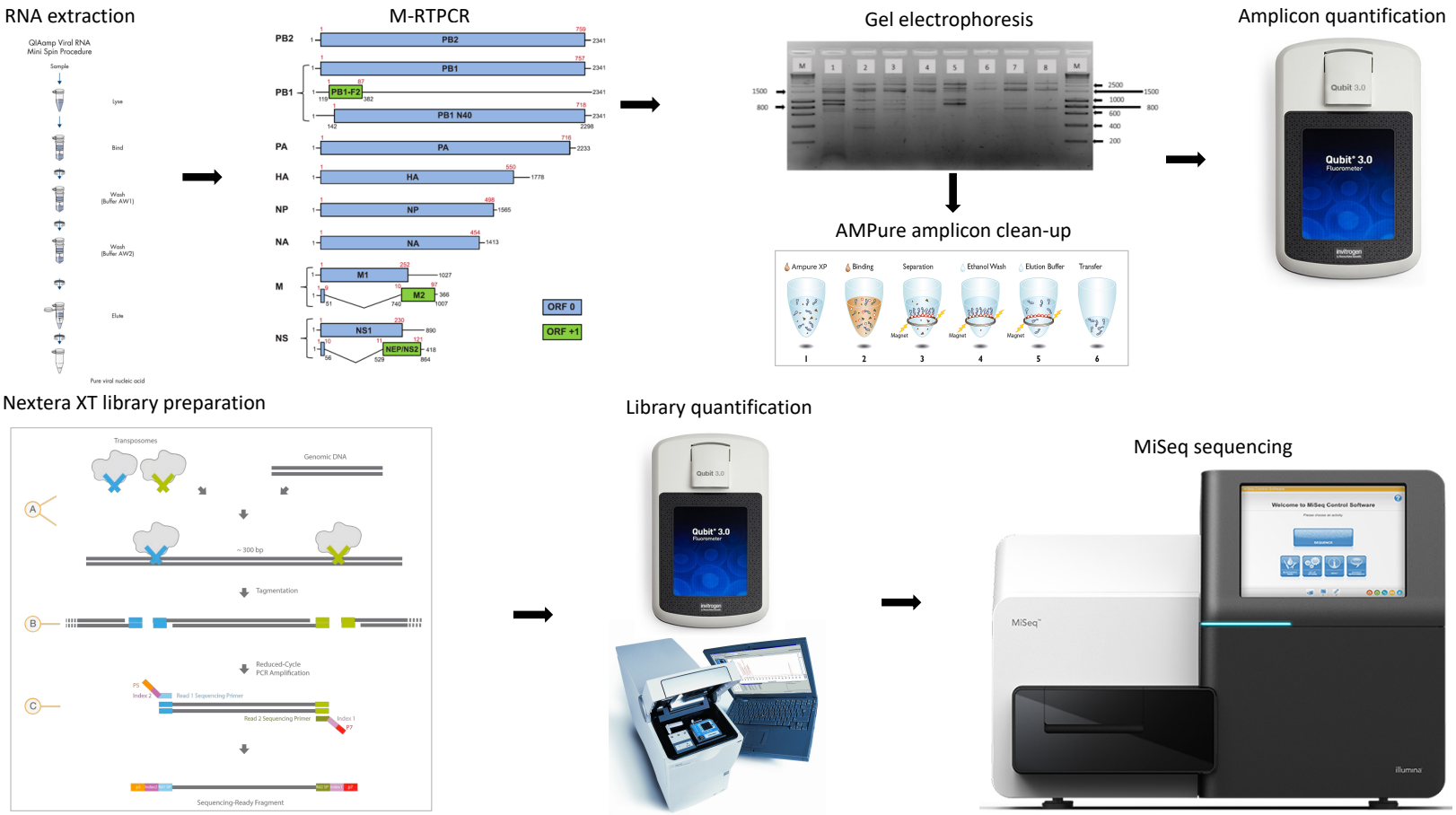


Figure 2.7: Sample preparation workflow showing: viral RNA extraction; M-RTPCR for amplicon generation and gel electrophoresis to confirm success of amplicon amplification; amplicon clean-up using AMPure beads; amplicon quantification using Qubit System; library preparation using Nextera XT kit; library quantification and fragment size evaluation using Qubit and BioAnalyzer Systems, respectively; and MiSeq sequencing.

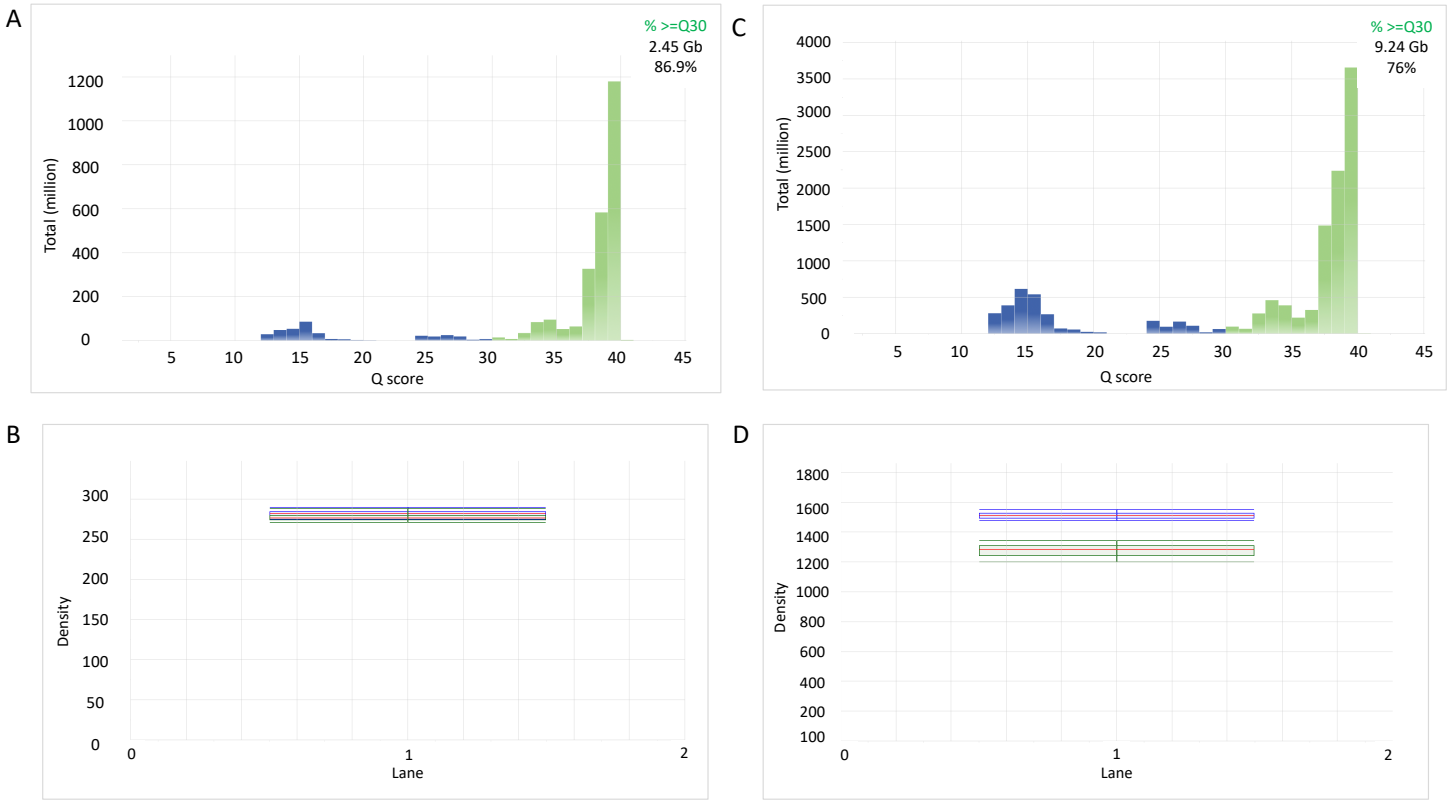


Figure 2.8: Run metrics for libraries generated by a 2 × 250 bp kit. Panels (A) and (B) are metrics for a library optimization run showing number of reads (million) with a Q-score (Q) range of 0-40 (A); Q30 and Q40 define 99.9% and 99.99% base call accuracy, respectively. Base calling quality was defined by Q-score; the higher the Q-score the accurate the base call. A total of 2.45 Gbases (Gb) or 86.9% of reads had Q-score ≥30 (expected yield is >75% bases with ≥Q30). The cluster density of 282 was very low (B) (normal range is 1000-1200 K/mm^2). Panels (C) and (D) are metrics for an optimized sequencing run showing 9.24 Gb or 76% of reads had Q-score ≥30 (C) with a cluster density of 1,250 K/mm^2 within range (D).

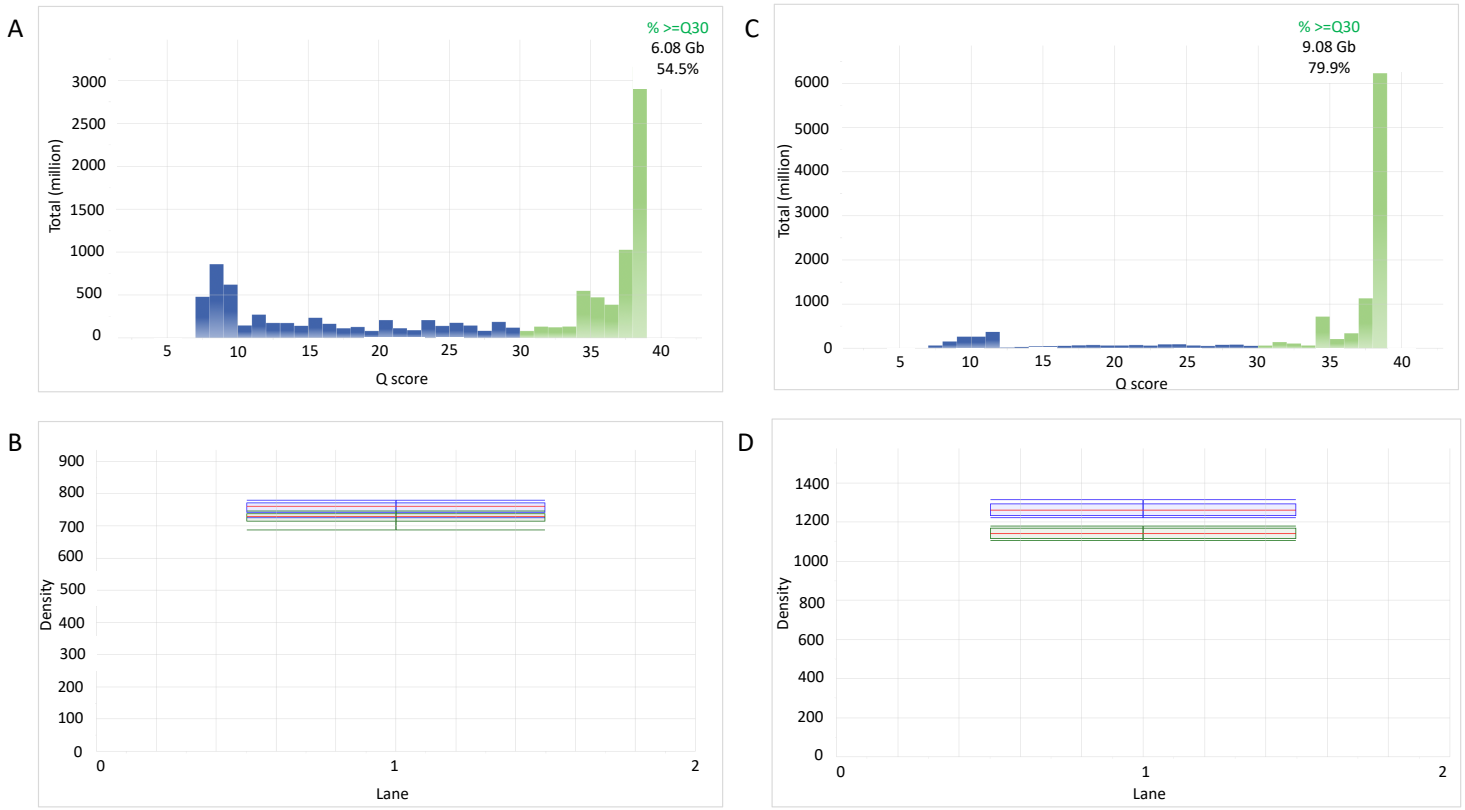


Figure 2.9: Run metrics for libraries generated by a 2 × 300 bp kit. Panels (A) and (B) are metrics for a library optimization run showing number of reads (million) with a Q-score (Q) range of 0-40 (A); Q30 and Q40 define 99.9% and 99.99% base call accuracy, respectively. Base calling quality was defined by Q-score; the higher the Q-score the accurate the base call. A total of 6.08 Gb or 54.5% of reads had Q-score ≥30: expected yield is >70% bases with ≥Q30. Cluster density of 756 was low (B) (normal range is 1200-1400 K/mm^2). Panels (C) and (D) are metrics for an optimized sequencing run showing ~9.08 Gb or 79.9% of reads had Q-score ≥30 (C) with cluster density of 1,310 K/mm^2 within expected range (D).

2.6 IAV Genome Assembly

2.6.1 Reference-Based and de novo NGS Assemblers

Although it is becoming easier and more feasible to utilize NGS to generate WGS data for IAV surveillance as described earlier (see Chapter 1, section 1.12), the diversity and mutation rate of IAV presents a challenge to high-throughput NGS genome assembly efforts. Assembly of IAV genomes from NGS short-read data is used to obtain full-length virus genomes. Reference-based NGS assemblers that map sequence reads to an available reference sequence were written for eukaryotic and prokaryotic organisms with non-segmented genomes that undergo slower mutation rates than RNA viruses (Watson et al., 2013; Wilm et al., 2012; Wright et al., 2011). However, these assemblers discard read sequences with too many mismatches or insertions/deletions (indels) in comparison to a defined reference sequence from assembly within some configurable scoring threshold (Shepard et al., 2016). Read sequences consisting of variants are more frequently discarded from reference-based assemblies due to an overall mismatch to the reference; it is therefore possible for thousands of acceptable reads to be excluded from the assembly, which minimizes the overall coverage and prevents complete assembly (Shepard et al., 2016). For highly variable viruses, like influenza, the use of a distant reference may cause variant calling errors due to misalignment of reads or incomplete assembly of genome fragments of high divergence (Fedonin et al., 2019; Iqbal et al., 2012). A common solution to the challenges observed with reference-based assemblers is to first assemble consensus sequence *de novo* (non-reference based assembly) and then use the resulting consensus sequence as a reference for mapping the reads and for variant detection using virus-specific *de novo* assemblers, for example, Vicuna (Yang et al., 2012) and Iterative Virus Assembler (Hunt et al., 2015). However, state-of-the-art *de novo* assemblers produce unique influenza virus genomes only 21% of the time (Hunt et al., 2015),

which means that they are poor candidates for high throughput NGS surveillance of RNA viruses (Shepard et al., 2016).

2.6.2 Evaluation of Reference-Based Assembly using Short-Read NGS Data from Kenya

High-throughput NGS short-read data can be mapped to a known reference genome in a reference-based assembly. Most mapping programs are Burrows-Wheeler transform (BWT)-based tools, which rapidly align reads to a reference genome using low computational resources (Orton et al., 2016), for example, BWA (Li and Durbin, 2009) and Bowtie2 (Langmead et al., 2009). Therefore, reference selection is an important step in this type of assembly; if the reference genome is too distantly related to the sample, mapping programs may struggle to map majority of the reads, resulting in poor or incomplete coverage (Orton et al., 2016). Most mapping tools utilize the Sequence Alignment Map (SAM) format (Li et al., 2009) to store all read mappings, which is usually converted into the Binary Alignment Map (BAM) format that holds the same data but in a binary format; this compresses the file and makes read sorting and indexing faster. SAMtools is a key tool, which provides various utilities for manipulating alignments in the SAM/BAM format including sorting, merging, indexing and generation of alignments in a per-position format (Li et al., 2009). For consensus calling, nucleotide differences (mutations and insertions/deletions) in the sample relative to the reference genome are first identified. SAMtools can be used in conjunction with VCFtools (Danecek et al., 2011) to identify variations from the reference genome (variants).

BWA program was evaluated in order to establish its suitability for assembly of short-read NGS data generated in this study from IAV. Ten paired-end read datasets from KNH (*Table 2.5*) were assembled using BWA program based on one of the earliest A(H1N1)pdm09 virus reference genome (A/California/07/2009). SAMtools was then used to sort, merge and index the files

followed by alignment. The assembly results are shown in *Figure 2.10*, which highlights the segments and segment positions where incomplete coverage was observed using BWA assembler. The assembly script, raw read output files, reference files, and assembly output files (small file sizes only) are available in the study's GitHub repository; (https://github.com/DCollinsOwuor/H1N1pdm09_and_H3N2_virus_genome_assembly_and_global_dataset_collation/tree/master/2_H1N1pdm09_virus_Kenya_reference-based_assembly).

Table 2.5: Details for short-read data for A(H1N1)pdm09 virus from KNH that were assembled using BWA.

Sample	GISAID Accession	Number of Reads	PCR Ct	Collection Date
KNH-1870	EPI_ISL_420557	356,713	23.47	10-Jul-2009
KNH-1892	EPI_ISL_420558	307,112	16.4	23-Jul-2009
KNH-1916	EPI_ISL_420559	279,794	17.1	29-Jul-2009
KNH-1931	EPI_ISL_420560	355,997	27.9	11-Aug-2009
KNH-1974	EPI_ISL_420561	512,867	20.19	12-Oct-2009
KNH-1987	EPI_ISL_420562	413,095	21.19	03-Nov-2009
KNH-2004	EPI_ISL_420593	510,128	24.44	25-Nov-2009
KNH-2005	EPI_ISL_420594	459,359	27.48	27-Nov-2009
KNH-2008	EPI_ISL_420595	262,594	26.39	30-Nov-2009
KNH-2011	EPI_ISL_420596	376,127	17.76	02-Dec-2009

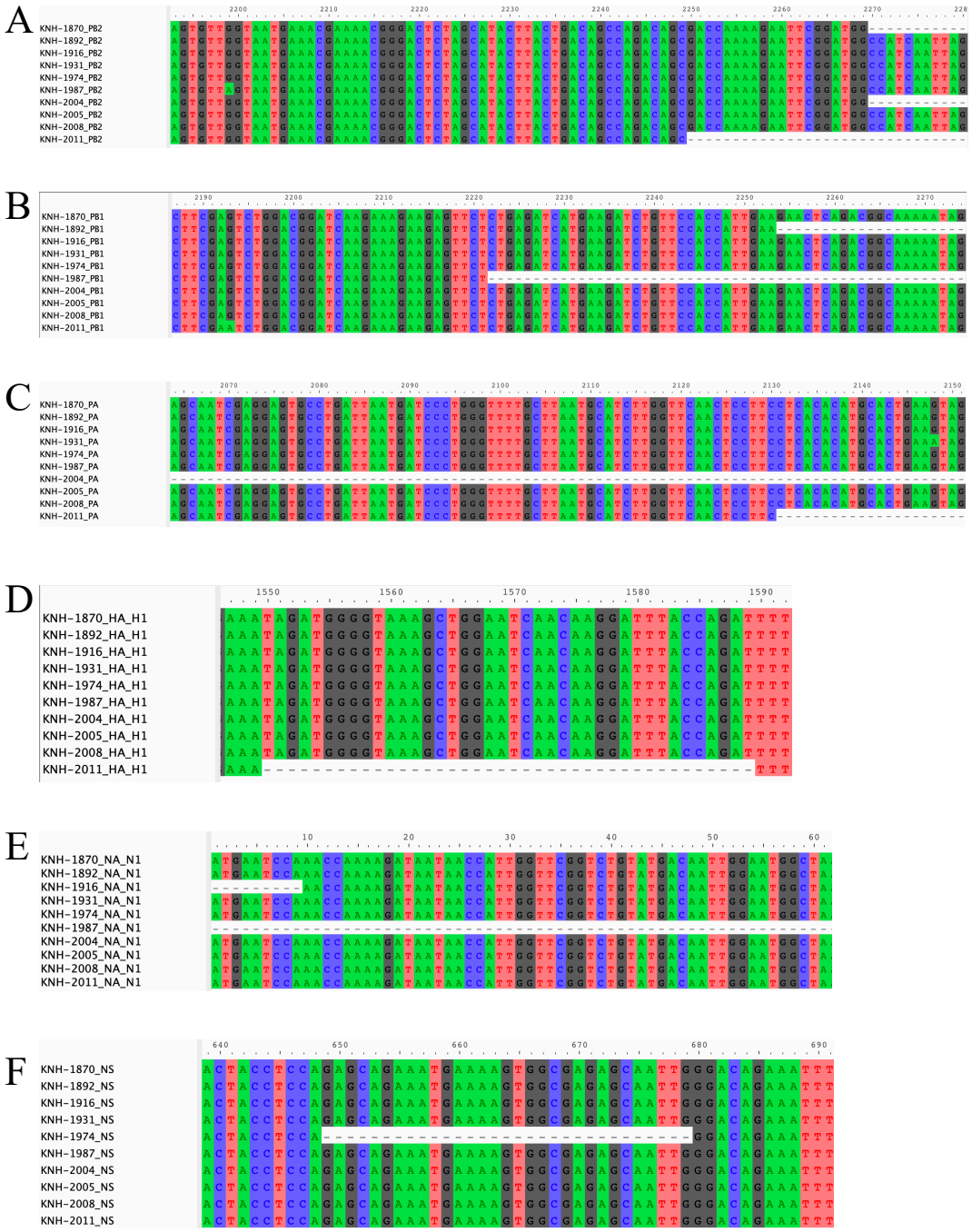


Figure 2.10: Evaluation of BWA assembler for short-read NGS data assembly from Kenya. Only segment positions with incomplete coverage i.e., missing nucleotides in PB2, PB1, PA, HA, NA and NS are shown.

BWT-based mapping programs rapidly align reads to a reference genome using low computational resources (Orton et al., 2016). In this assembly evaluation, a MacBook Pro laptop with a 2.8 GHz processor and 8 GB of Random-Access Memory (RAM) was used. The assembly of the 10 paired-end reads took ~3 hours. Thus, the computational speed of BWA was confirmed in this evaluation. However, the BWT-based mapping programs may struggle to map majority of reads, resulting in poor or incomplete coverage (Orton et al., 2016; Shepard et al., 2016). Additionally, the diversity and mutation rate of IAV presents a challenge to high-throughput NGS assembly efforts as it limits the choice of reference genomes for use in the reference-based assembly (Orton et al., 2016). The reference-based assemblers discard read sequences from assembly which have too many mismatches or insertions/deletions in comparison to the reference (Orton et al., 2016; Shepard et al., 2016). There were portions of the genome segments with incomplete coverage; majority of the incomplete sequence positions occurred at the start (first 70 nucleotides) and at the ends (last 90 nucleotides) of the genome segments as shown in *Figure 2.10*. Incomplete coverage could be due to read sequences composed of variants being discarded from the assembly because of the overall mismatch to the reference; it is therefore possible that thousands of acceptable reads (of sufficient length and quality based on Q-scores) were excluded from the BWA assembly, which minimized the overall coverage and prevented complete IAV genome assembly (Orton et al., 2016; Shepard et al., 2016).

2.6.3 Iterative Refinement Meta-Assembler (IRMA)

As shown in the BWA assembly exercise, common reference-based assemblers do not perform universally well for segmented viruses that undergo rapid evolution and reassortment, for example, influenza virus. Therefore, IRMA software (Shepard et al., 2016) was developed as a flexible approach to address viral diversity. It is routinely used to process genome sequence data generated

from the large volume of influenza surveillance specimens at USA CDC Influenza Genomics team. IRMA is a meta-assembler, which provides segment level read sorting based on Lineage Assignment By Extended Learning (LABEL), a sequence classification tool ideal for segmented genomes (Shepard et al., 2014). IRMA iteratively gathers reads and iteratively edits the reference templates to account for high population diversity and mutational rates, and provides redesigned variant calling and phasing to allow for analysis of diverse virus sub-populations. IRMA automates quality control, such as removal of short, low quality and chimeric reads. Additionally, IRMA parallelizes tasks at each analysis step by using multi-core computer or by grid, which enables handling of high-volume sequence assembly and analysis using maximum computational capability (Shepard et al., 2016).

In the IRMA pipeline (*Figure 2.11*), iterative refinement involves moving the reference template closer to the reads (editing references using reads iteratively) to obtain quality assemblies with increased sensitivity to distant and novel genetic variants. Iterative refinement of references to optimize the final assembly is based on the Striped Smith-Waterman (SSW) algorithm (Zhao et al., 2013). The first phase (steps 1-5) of the IRMA pipeline focuses on gathering as many NGS reads as possible by matching them to reference sequences, sorting them into their respective gene segments, and using the results of a rough alignment to edit the references. Any unmatched reads go back into the pool for additional rounds of matching after the references are refined. This step ensures that unmatched reads are not necessarily discarded because of the use of genetically distant reference sequences. The second phase (steps 6-9) of the pipeline finalizes the assemblies by iteratively editing references in order to find an optimal assembly score; afterwards, read pairs may be merged, statistics tabulated, variants called, and figures drawn (Shepard et al., 2016).

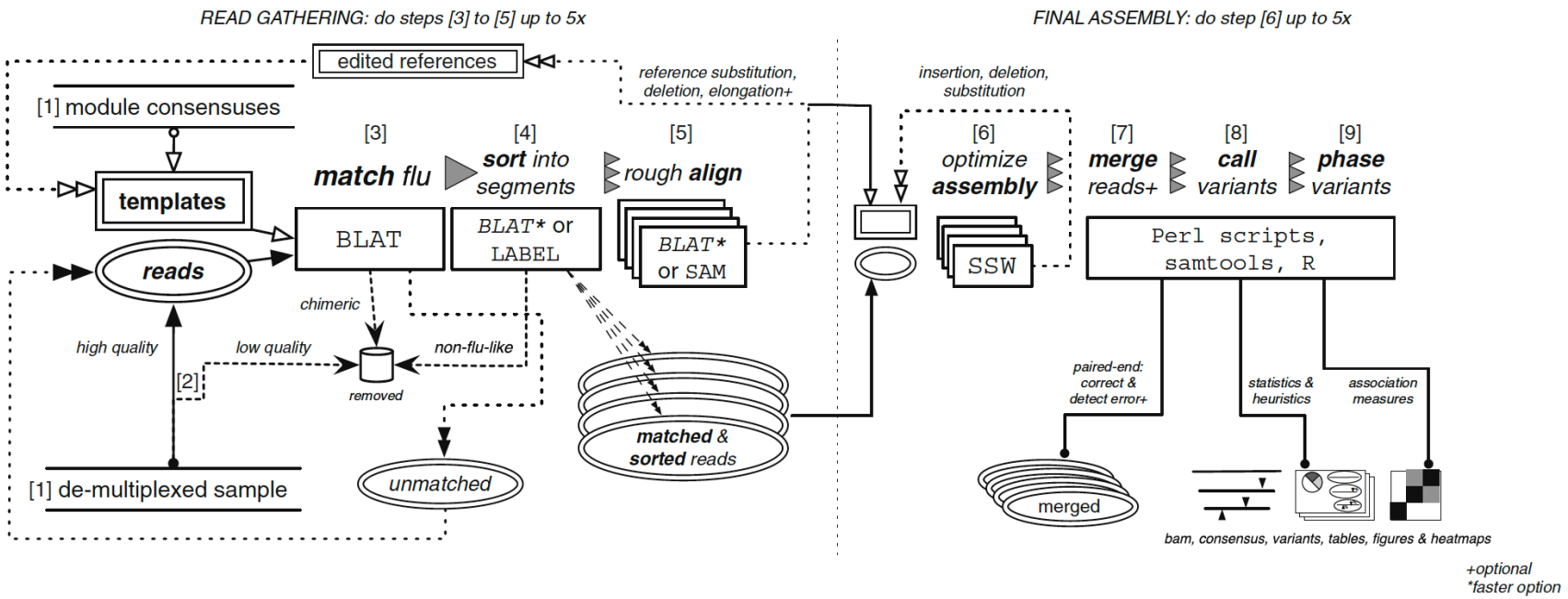


Figure 2.11: Iterative Refinement Meta-Assembler (IRMA) workflow adapted from (Shepard et al., 2016). The IRMA pipeline showing the iterative process, which involves read gathering (steps 1-5) and finalization of the assembly by iteratively editing references (steps 6-9) process.

2.6.4 Genome Assembly of NGS Short-Read Data from This Study Using IRMA

Contiguous (contigs) nucleotide sequence assembly was carried out using the FLU module of IRMA (Shepard et al., 2016). IRMA quality control, variant calling and phasing, and assembly pipelines were all implemented in the EDGE Bioinformatics environment (Li et al., 2017) to utilize IRMA's task parallelization using multi-core high-throughput computing. The assemblies were conducted using IRMA default settings: median read Q-score filter of 30; minimum read length of 125; frequency threshold for insertion and deletion refinement of 0.25 and 0.6, respectively; Smith-Waterman mismatch penalty of 5; and gap opening penalty of 10. All the sequence data were deposited in GISAID EpiFlu^{TM} database with the accession numbers available in *Appendix 7.2.1* (influenza A(H1N1)pdm09 Virus, Kenya, 2009-2018)*, Appendix 7.2.2* (influenza A(H3N2) Virus, Kilifi, Kenya, 2015-2016), and *Appendix 7.2.3* (influenza A(H1N1)pdm09 and A(H3N2) Viruses, PERCH-Africa, 2011-2013). Assembly results for the 10 paired-end short-read data from KNH, which were initially assembled using the BWA assembler to evaluate the reference-based assembly (section 2.6.2) are shown in *Figure 2.12*. IRMA generated full-length and complete coverage of all the genome segments, which had generated incomplete genome coverage with the BWA assembler. The IRMA assembly output is available in the study's GitHub repository; (https://github.com/DCollinsOwuor/H1N1pdm09_and_H3N2_virus_genome_assembly_and_global_dataset_collation/tree/master/3_H1N1pdm09_virus_Kenya_IRMA_assembly).

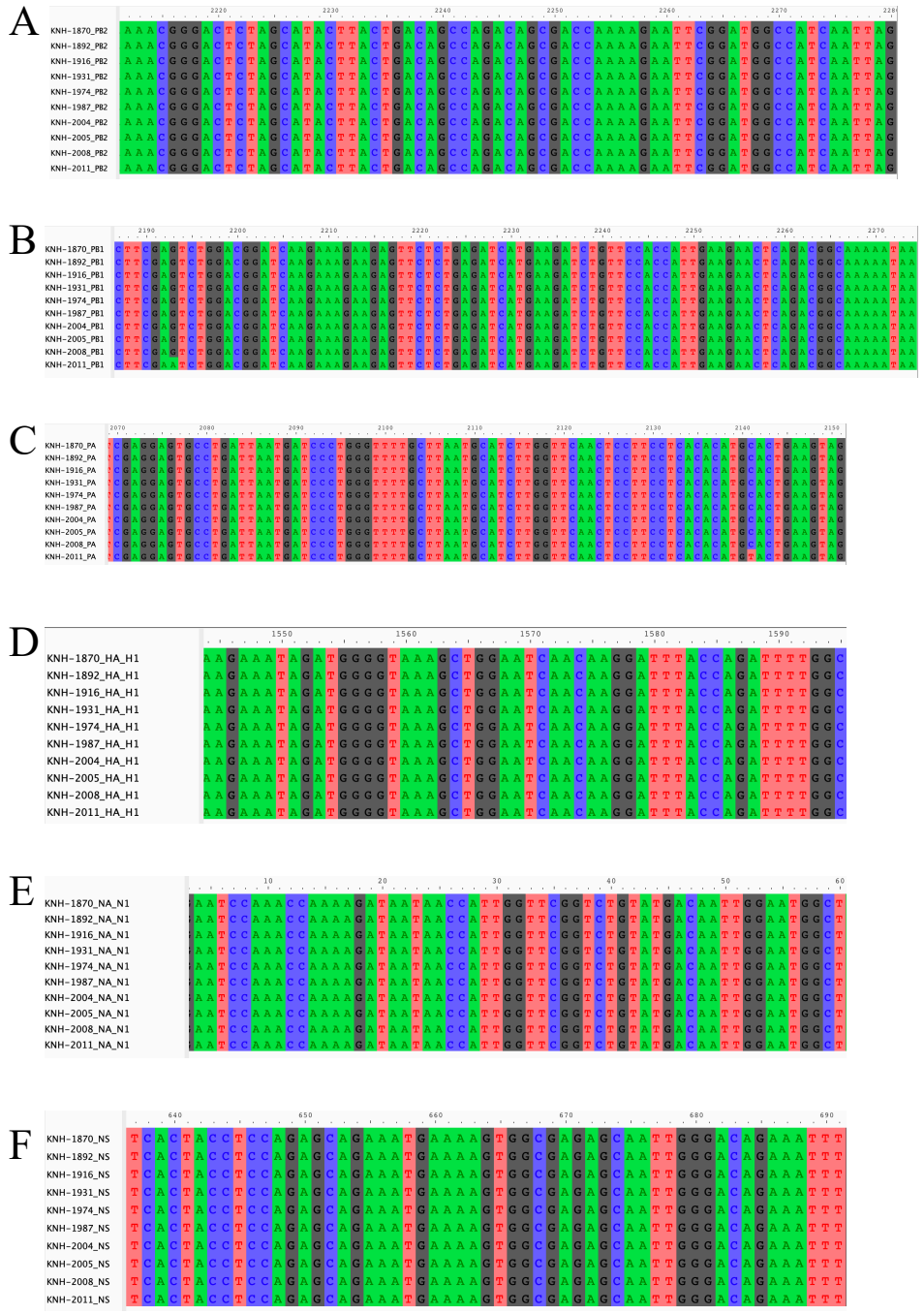


Figure 2.12: Assembly of short-read NGS data from Kenya using IRMA. Segment positions that had incomplete coverage with BWA assembler are displayed to show complete coverage achieved with IRMA.

2.7 Global Influenza A(H1N1)pdm09 Virus and A(H3N2) Virus Dataset Collation

2.7.1 Global Initiative on Sharing All Influenza Data (GISAID)

Global IAV genomes were obtained from the GISAID (https://platform.gisaid.org/epi3/cfrontend) database. The GISAID Initiative promotes the rapid sharing of data from all influenza viruses. The database contains genetic sequence and related epidemiological and clinical data associated with all influenza viruses. The sharing of the data aims to help researchers understand the evolution and spread of influenza viruses during epidemics and pandemics. GISAID's publicly accessible EpiFlu^{TM} database ensures that open access to the data is free-of-charge to all users who have agreed to uphold GISAID's data sharing guidelines upon registration. The registered users with access credentials agree to uphold scientific etiquette by acknowledging the originating laboratories providing the specimens and the submitting laboratories generating virus sequence data and other metadata and ensuring fair utilization of results derived from the data. GISAID also requires that users agree that no restrictions shall be attached to the data submitted to the database, which promotes collaboration among researchers through open sharing of data. Public Domain archives, for example, the National Center for Biotechnology Information's (NCBI) GenBank and Virus Pathogen Database and Analysis Resource (ViPR) databases, where access and use of data takes place anonymously, neither offers any protection of the owners' intellectual property rights to the data or additional incentive for sharing data, such as transparency on the use of data. Additionally, the Public Domain archives lack effective mechanisms that would ensure the acknowledgment of the owners of the data and recognition of the data submitters. These hurdles in the Public Domain archives necessitated the formation of the GISAID platform to address these concerns, which was launched on the occasion of the Sixty-first World Health Assembly in May 2008. Since its launch, GISAID plays an important role in the sharing of data among the WHO

Collaborating Centers and NICs for the bi-annual influenza vaccine virus recommendations by the WHO's GISRS.

The GISAID database provides features for searching virus sequences, filtering datasets for download and data upload functionality. All updated sequence data are submitted through a rigorous curation process. The main features of the platform include: storage of influenza virus sequences and associated metadata; availability of genetic, clinical, epidemiological and geographical data for human virus isolates and species specific data associated with non-human isolates; real-time batch and single upload functionality; ability of users to edit already submitted data; immediate availability of submitted data to the public; download capability of metadata associated with isolates; and sequence download in fasta file format. The database has the largest collection of curated virus sequence data, for example, there were 805,666 sequences from 321,398 influenza virus isolates as of 4th June 2020 (https://platform.gisaid.org/epi3/cfrontend).

2.7.2 Collation of Global A(H1N1)pdm09 Virus and A(H3N2) Virus Datasets

A number of comparison datasets for influenza A(H1N1)pdm09 virus and A(H3N2) virus from GISAID were prepared that would provide a phylogenetic context of the sequences from this study (*Figure 2.13*). This would improve understanding of the sequence data from this study by providing a global contemporaneous comparison dataset, which would provide phylogenetic context to the sequences generated in this study. This was conducted to determine the relatedness of the viruses in this study to those circulating around the world and hence understand their global context. Due to the large collection of sequences of influenza viruses in the GISAID database, a methodical approach was used to select a final collection of ~1,500 global WGS data for both A(H1N1)pdm09 and A(H3N2) viruses; there were 14,233 WGS data for A(H1N1)pdm09 virus generated from virus isolates collected from March 2009 to December 2018 and 11,058 WGS data

for A(H3N2) virus generated from virus isolates collected from January 2009 to December 2016 as of 4th June 2020. Since the goal of this study was to conduct in-depth phylogeographical inference of IAV, it was important to consider the number of global and local sequences in the final phylogeographical analyses. Due to the large number of parameters that are estimated in Bayesian phylogeographic studies, the analysis is slow for larger datasets and the number of distinct states is also limited (Reimering et al., 2020). The selection is not a total random process but aims to be as spatially and temporally representative as possible depending on the sequence dataset under analysis. In summary, the key challenges in undertaking the rigorous selection were: (i) large number of genomes in GISAID database to select from; (ii) limited computational power anticipated when dealing with large datasets for Bayesian phylogeographic analyses; and (iii) uneven spatial and temporal distribution of the virus sequence data.

The methodical approach for selecting the final virus genome dataset included: removal of duplicate sequences, removal of sequences with missing dates (collection date, month, and year), removal of incomplete sequences, removal of sequences with ambiguous nucleotides (N), and removal of incomplete sequences; *Figure 2.13*. Representative sequences were binned by year and continent. For geographic regions with large datasets, intermittent sequences were randomly selected using in-house scripts; https://github.com/DCollinsOwuor/H1N1pdm09_and_H3N2_virus_genome_assembly_and_global_dataset_collation. For example, for A(H3N2) virus, North America has the largest number of publicly available WGS data (n=4,511) after cleaning. From these, 428 WGS data were randomly sub-sampled and stratified by 2 time periods (2010-13 and 2014-16) for 2 separate phylogeographic analyses, respectively; *Figure 2.13*. For under-represented geographic regions, all available WGS datasets were included to overcome ascertainment bias. For example, for

A(H3N2) virus, Africa has the lowest number of publicly available WGS (n=288) after cleaning. Therefore, all African WGS data were included in the final dataset and stratified by 2 time periods (2010-13 and 2014-16); *Figure 2.13*. Full-length WGS data from IAV isolates collected from March 2009 to December 2018 for A(H1N1)pdm09 virus and from January 2010 to December 2016 for A(H3N2) virus from the 6 continents were downloaded. Only complete WGS datasets were included to improve the phylogenetic resolution of the Bayesian phylogeographic analyses. The data were organized into a Microsoft Excel database, which also stored the associated metadata (country of origin, date of isolation, subtype, originating and submitting laboratories, and sequence lengths for each of the 8 segments). Subsets of the data were extracted depending on the research question to be addressed as described in the subsequent data chapters.

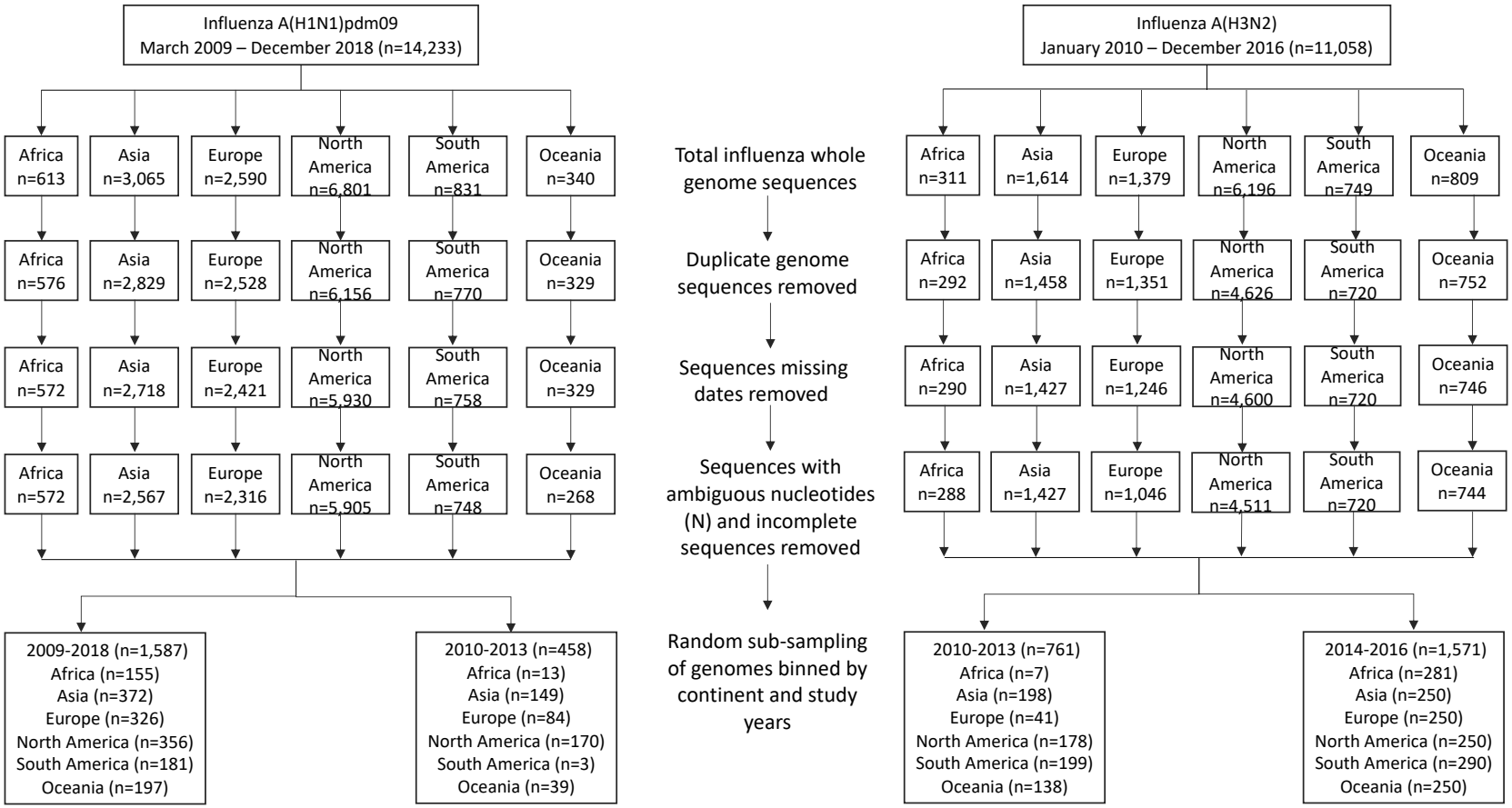


Figure 2.13: Global dataset selection for IAV from GISAID showing the selection process for whole-genome sequences, which included removal of duplicate sequences, sequences with missing dates (collection date, month, and year), and sequences with ambiguous nucleotides (N). Representative sequences were binned by year and country. For geographic regions with large datasets, intermittent sequences were randomly selected using in-house scripts. For under-represented regions, all available WGS data were included to overcome ascertainment bias.

CHAPTER THREE

3 Phylogeography of Influenza A(H3N2) Virus in Kilifi, Kenya, 2015-2016

3.1 Introduction

The global surveillance of influenza viruses has resulted in the generation of a uniquely extensive collection of geographically and temporally comprehensive virus sequences, which has provided an opportunity to explore the drivers of global circulation of influenza viruses (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2009b; Nelson et al., 2006; Rambaut et al., 2008; Russell et al., 2008). However, the role of tropical/sub-tropical low-to-middle income countries in the global migration dynamics of influenza viruses remains unclear due to insufficient data (Ng and Gordon, 2015; Viboud et al., 2013) especially in sub-Saharan Africa despite the high disease burden especially in children under the age of 5 years, the elderly persons aged ≥65 years and older, pregnant women, and individuals with chronic medical and immunosuppressive conditions (Gessner et al., 2011; Katz et al., 2012b; Wang et al., 2020).

An important epidemiological question is whether a global source population of influenza virus exists in tropical and sub-tropical Africa. Most analyses on the existence of a global source population of influenza have focused on E-SE Asia, attributed in part due to the apparent origins of several pandemics and seasonal epidemics in those regions (Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2014; Russell et al., 2008). For example, studies have shown that globally, annual A(H3N2) virus epidemics result from the introduction of new genetic variants from E-SE Asia, where viruses circulate via a network of temporally overlapping epidemics (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2014; Russell et al., 2008) rather than local persistence (Nelson et al., 2007; Nelson et al., 2006; Rambaut et al., 2008; Russell et al., 2008). Therefore, the global persistence of A(H3N2) virus results from temporally migrating virus

metapopulations (multiple influenza virus populations or lineages, which result from temporally overlapping epidemics in multiple global regions) in which new virus strains can emerge in any geographical region, with the location of the source population changing regularly (Bahl et al., 2011). These studies, which have aimed to infer the location through time of the 'source' population of A(H3N2) virus, mostly concluded that the virus resides primarily in E-SE Asia (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2014). However, temperate regions particularly the USA have also been shown to possibly contribute as a source (Bahl et al., 2011; Bedford et al., 2010) and there is evidence for viral gene flow into Asia from elsewhere, for example, USA and China (Bahl et al., 2011; Bedford et al., 2015). These studies suggest that multiple lineages may seed annual influenza epidemics, and that multiple regions may act as a potential source population for influenza virus epidemics (Bahl et al., 2011) including tropical and sub-tropical Africa.

Therefore, a more complete understanding of the global circulation of influenza viruses requires deeper and wider sampling from understudied tropical and sub-tropical regions notably Africa, India, and Latin America (Viboud et al., 2013). For example, additional analysis of influenza surveillance data from India led to the discovery that the global source region for A(H3N2) viruses also includes India in addition to E-SE Asia (Bedford et al., 2015). Identifying a geographical source of new antigenic and genetic variants of influenza viruses could potentially improve early detection and prediction of new vaccine strains (Viboud et al., 2013). Because of the insufficient spatiotemporally representative sequence data of influenza viruses from tropical and sub-tropical African countries, relatively little is known about the possible role the region plays in the global migration of influenza viruses (Byarugaba et al., 2016; Dia et al., 2013; Gachara et al., 2016; Nelson et al., 2014). For example, little is known about the role of Africa as a source of new genetic

and antigenic variants that seed global epidemics and their patterns of persistence. Non-molecular epidemiological studies have hinted at climate-driven patterns of influenza virus spread in Africa, for example, in Kenya (Emukule et al., 2016) and Uganda (Yang et al., 2018), where climatic factors have been shown to influence the activity of influenza viruses. Africa's diverse climates make it an ideal location to investigate its role as a global source population of influenza viruses since persistence in such African countries might be facilitated by climatic variability, which can generate temporally overlapping epidemics in neighboring regions (Nelson et al., 2014), patterns which have been associated with global migration of influenza viruses and persistence of viruses in E-SE Asia (Bahl et al., 2011). Additionally, some countries in Africa are known to experience year-round (or multi-annual) influenza activity, for example, Kenya, Burkina Faso, Ghana, and Nigeria (Hirve et al., 2016; Newman et al., 2018), which makes it an ideal location to investigate virus persistence patterns and subsequent global seeding of influenza viruses.

Several prospective, hospital- and community-based surveillance cohorts were established in multiple regions of Kenya, providing a unique opportunity to examine the epidemiology of human influenza viruses (Emukule et al., 2014; Emukule et al., 2019; Katz et al., 2012a; Katz et al., 2014; Nyiro et al., 2018). The objective of the study was to determine the patterns of spread of IAV in Kilifi, a coastal region of Kenya and the origins of the viruses seeding A(H3N2) virus epidemics at the local Kilifi level. No phylogeographic analysis of influenza viruses has been conducted in Kenya before. The analysis was based on human influenza A(H3N2) virus owing to its frequency and severity associated with seasonal epidemics globally (Westgeest et al., 2014). A(H3N2) virus remains a significant cause of influenza in Kenya (Katz et al., 2014; Onyango et al., 2012a; Owuor et al., 2020), is a dominant virus subtype in other regions of the world and causes substantial morbidity and mortality in Kenya and beyond. A key aspect of this study is that it involved

continuous, active, year-round surveillance that enabled capture of any inter-seasonal strains. The analysis of local and global sequence data provided an improved phylogenetic resolution to describe the global patterns of spread of A(H3N2) virus and the source population of virus introductions into Kilifi, Kenya.

3.2 Materials and Methods

3.2.1 Local (Kilifi) Sample Details and Sequencing

Samples were collected from health facilities within the KHDSS on the coast of Kenya (see Chapter Two, section 2.3.4 for a full description of the study and sample details). Non-residents and residents of KHDSS presenting to these facilities were included. In total, 5,796 NP swab samples were taken from outpatients of all ages presenting with acute respiratory illness to a selected 9 primary health facilities spread throughout the KHDSS, from December 2015 to December 2016. Initial sample screening for 15 respiratory virus targets (including IAV), nucleic acid extraction, IAV genome amplification, and IAV genome assembly was performed as described in Chapter Two (sections 2.5.1, 2.5.2, 2.5.3, and 2.6.4).

3.2.2 Global Sequence Dataset Collation

Global WGS data of A(H3N2) virus used in these analyses were all retrieved from the GISAID EpiFlu^{TM} database (https://platform.gisaid.org/epi3/cfrontend/) and processed as described in Chapter Two, section 2.7.2. A final dataset of 1,571 global sequences sampled from January 2014 to December 2016 was assembled (numbers in parenthesis indicate number of sequences): Africa (281); Asia (250); Europe (250); North America (250); South America (290); Oceania (250).

3.2.3 Phylogenetic Analysis

Consensus nucleotide sequences were aligned and translated in AliView v1.26 (Larsson, 2014). The individual genome segments were concatenated into full-length genomes using SequenceMatrix v1.8 (Vaidya et al., 2011). Phylogenetic trees of A(H3N2) virus WGS data from Kilifi were constructed with maximum-likelihood and bootstrap analysis of 1,000 replicates (to evaluate the robustness of the phylogenetic clustering) based on best-fit nucleotide substitution models inferred using IQ-TREE v1.6.11 (Kalyaanamoorthy et al., 2017; Nguyen et al., 2014) and chosen by the Bayesian Information Criterion (BIC) for each concatenated virus genome. The phylogenetic trees were visualized and annotated using Figtree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). The full-length HA sequences of all the virus genome sequences were used to characterize A(H3N2) virus strains into genetic groups (i.e., clades, subclades, and subgroups) according to the European CDC Guidelines (https://www.ecdc.europa.eu/en/seasonal-influenza/surveillance-and-disease-data/influenza-virus-characterisation) and PhyCLIP (Han et al., 2019), which uses linear integer programming to assign sequences into genetic groups.

3.2.4 Detection of Reassortments

Tanglegrams were reconstructed for multiple pairs of A(H3N2) virus gene segment phylogenies using Nextstrain (Hadfield et al., 2018) to visualize similarities and differences between the phylogenetic tree pairs and detect reassortments. The two phylogenetic tree pairs were visualized as time-resolved trees in a side-by-side conformation and connection lines between taxa that correspond to each other in the two trees were drawn to visualize similarities and differences in placement of viruses in the trees. The tanglegrams were generated based on HA phylogeny, which is used to characterize A(H3N2) virus strains into genetic groups, and whose topology is used to

map the phylogenetic leaf nodes and show reassortants when there is interchange of leaf node positions of virus genetic groups. The concatenated full-length genomes, which generated a single sequence for each A(H3N2) virus, based on sequences of all the eight gene segments, were used to reconstruct a whole-genome phylogenetic tree that was annotated by genetic group using ggtree (Yu et al., 2017).

Reassortment events were verified computationally using the Graph-incompatibility-based Reassortment Finder (GiRaF) tool (Nagarajan and Kingsford, 2011). GiRaF tool computationally maps reassortants onto phylogenetic trees, which initially involves down sampling of posterior samples of phylogenetic trees generated using Bayesian Evolutionary Analysis Sampling Trees (BEAST) and subsequent analysis to identify inter- and intra-subgroup reassortment events. In principle, every reassortment event must split all eight segments into two subsets (retained segments and acquired segments); however, for some reassortment events the phylogenetic signal may be too weak for some segments to be assigned to one of these two reassorting sets of segments. Therefore, as advised by the authors, a threshold of three pairwise comparisons resulting in at least four segments being placed confidently into either group was conducted with a confidence level >0.95 used for each pairwise comparison between segments that contributed to the detection of the reassortment event (Nagarajan and Kingsford, 2011).

3.2.5 Spatial Dynamics of A(H3N2) Virus Spread and Ancestral State Reconstruction

Phylogeographical analysis was conducted to assess virus migration between the KHDSS locations and in relation to the rest of the world using methods implemented in BEAST v1.10.4 package (Suchard et al., 2018). The analysis was implemented with an asymmetric discrete trait approach and applied the Bayesian stochastic search variable selection (BSSVS) model (Lemey et al., 2009a). To reduce the complexity of the maximum clade credibility (MCC), location states were

also categorized as “Kilifi” or “non-Kilifi”. Phylogeographic inferences were visualized with the Spatial Phylogenetic Reconstruction of Evolutionary Dynamics using Data-driven Documents (SPREAD3) v0.9.7.1c package (Bielejec et al., 2016). To visualize the geographic spread of the virus over time, a D3 file was generated using SPREAD3 v0.9.7.1c package. A KHDSS geo.json file was used for visualization and resulting log files were used to calculate Bayes Factor (BF) values for significant migration rates between discrete locations. The 2 discrete states (“Kilifi” or “non-Kilifi”) were used for ancestral state reconstruction for the geographical region of internal nodes of phylogenies using Kilifi and contemporaneous global sequences from other countries to detect virus introductions into Kilifi from time-resolved phylogenies in TreeTime (Sagulenko et al., 2018).

The potential transmission networks within and between populations visiting the enrolled KHDSS health facilities were inferred in Population Analysis with Reticulate Trees (PopART) package v1.7.2 (Leigh et al., 2015) using Templeton, Crandall and Sing (TCS) method with an epsilon of zero. These networks were created for all of the Kilifi A(H3N2) viruses from the concatenated segment alignments.

3.2.6 Bayesian Tip-association Significance (BaTS) Test

The strength of geographical clustering for viruses from Kilifi was assessed using the phylogeny-trait association test implemented in the BaTS package (Parker et al., 2008). Each virus genome sequence was assigned a geographic code reflecting its place of origin within the KHDSS. The overall statistical significance of geographical clustering of all Kilifi sequences was determined by calculating observed and expected association index and parsimony score statistics, where the null hypothesis is that clustering by geographical location is not more than that expected by chance. Additionally, the maximum clade statistic was used to compare the strength of clustering at each

of the KHDSS location by calculating the expected and observed mean clade size from each of the 9 outpatient locations. A significance level of $p \leq 0.05$ was used in all scenarios.

Analysis files and scripts can be found on the study's GitHub repository: https://github.com/DCollinsOwuor/H3N2_virus_Kilifi_phylogeography.

3.3 Results

3.3.1 IAV Whole-Genome Sequencing and Assembly

A total of 5,796 NP swab samples were tested from outpatients of all ages presenting with ARI to selected 9 outpatient health facilities spread throughout the KHDSS from December 2015 to December 2016. A total of 97 IAV positive specimens were detected from the outpatient health facilities. Of the 97 IAV positive specimens identified for this study, 96 (98.9%) were retrieved; the remaining sample had too little residue for RNA extraction i.e., less than 140 µL. Of these 96 specimens, 72 (75%) that passed pre-sequencing quality control checks (see Chapter Two, section 2.5.3 for the quality control methods for IAV amplicons and libraries) were loaded onto the Illumina MiSeq with corresponding success in generating WGS data for 66 (91.7%) specimens. The 24 samples that failed quality control checks had low amplicon concentrations for library preparation. A total of 58 (92.1%) A(H3N2) virus WGS data were generated comprising 4 genetic groups from samples collected from December 2015 to December 2016: clade 3C.2a (n=34, 58.6%); subclades 3C.2a2 (n=3, 5.2%) and 3C.2a3 (n=1, 1.7%); and subgroup 3C.2a1b (n=20, 34.5%) (*Appendix 7.2.2*). Between 50,000 and 420,000 short-read sequences were available per sample of which IAV-specific reads ranged between 9,000 to 400,000 reads (each of 250 bases); *Appendix 7.2.2*. All the genome assemblies were 13,133 nucleotides in length with mean depth of base coverage per genome ranging from 170 to 7,600 (calculated from, for example, [400,000 reads X 250 bases]/13,133). With regard to sequence availability in GISAID, these are among the

first set of A(H3N2) virus WGS data from Kilifi, Kenya. Therefore, they make an important contribution to the available sequences from Kenya that can be used to understand the local evolutionary and transmission dynamics of IAV. The socio-demographic characteristics of these patients are shown in *Table 3.1*.

Table 3.1: Socio-demographic characteristics of the Kilifi Health and Demographic Surveillance System (KHDSS) outpatients.

		Outpatient (KHDSS)	
		n	%
Age	0-11 mths	9	(15.52)
	12-59 mths	18	(31.04)
	6-15 yrs	15	(25.86)
	16-64 yrs	13	(22.41)
	>=65 yrs	3	(5.17)
Gender	Female	26	(44.83)
	Male	32	(55.17)
Cough	No	2	(3.45)
	Yes	56	(96.55)
Breathing difficulty	No	53	(91.38)
	Yes	5	(8.62)
In-drawing	No	53	(91.38)
	Yes	5	(8.62)
Unable to feed	No	56	(96.55)
	Yes	2	(3.45)
Oxygen saturation	<90	2	(3.45)
	>=90	56	(96.55)
Conscious level	Alert / Normal	56	(96.55)
	Lethargic	2	(3.45)
	Prostrate	-	-
	Unconscious	-	-

3.3.2 Seasonality and Representativeness of Sequenced Samples

IAV was detected throughout the surveillance period in coastal Kenya (except in July, August, and September 2016) with the number of observed cases fluctuating from month-to-month, *Figure 3.1*. The different health facilities experienced peak incidences in different months of the surveillance, but majority fell between December 2015 and February 2016, and in November 2016. The proportion of samples from each health facility that were sequenced roughly reflected the overall distribution of positives that were detected in the specific health facilities, *Figure 3.2*. The sequencing of at least 1 sample from the 9 primary health facilities within the KHDSS allowed for interrogation of the transmission between populations served by these facilities. Clade 3C.2a and subgroup 3C.2a1b viruses were detected in most of the health facilities (8 and 6 of the 9 health facilities, respectively), which suggests that A(H3N2) viruses were in circulation throughout Kilifi without geographical restriction to a particular lineage during 2015-16, *Figure 3.3*. Subclades 3C.2a2 and 3C.2a3 viruses were characterized by 3 and 1 A(H3N2) virus detections, respectively which is consistent with limited local transmission of the subclades.

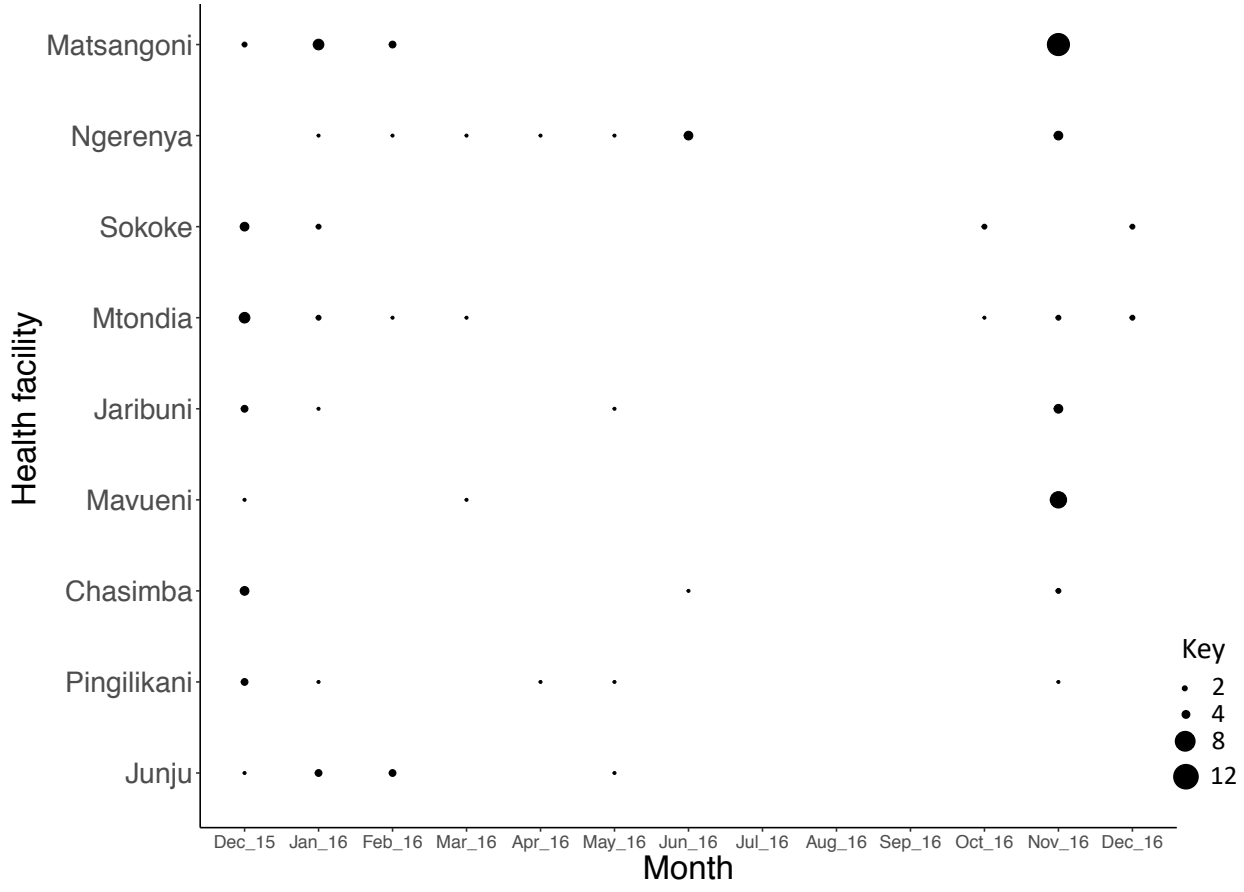


Figure 3.1: A bubble plot showing the number of IAV positives by month and health facility detected in the Kilifi surveillance from December 2015 to December 2016. The distribution of IAV positive samples was as follows: December 2015, n=23; January 2016, n=15; February 2016, n=8; March 2016, n= 3; April 2016, n=2; May 2016, n=4; June 2016, n=5; October 2016, n=3; November 2016, n=32; and December 2016, n=4. IAV, influenza A virus.

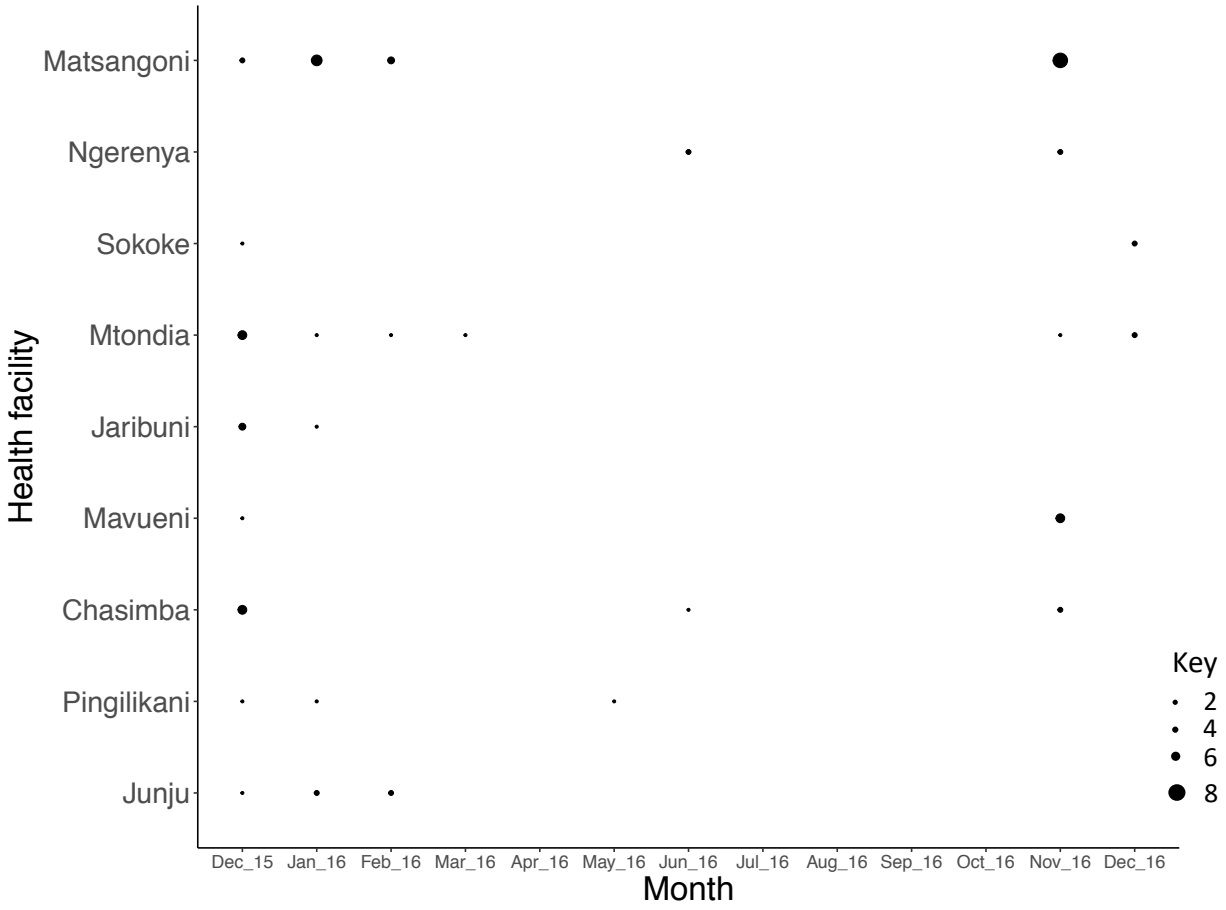


Figure 3.2: Bubble plot showing the number of IAV positives by month and health facility that were sequenced from Kilifi. The distribution of sequenced A(H3N2) virus positive samples was as follows: December 2015, n=15; January 2016, n=10; February 2016, n=6; March 2016, n=1; May 2016, n=1; June 2016, n=3; November 2016, n=16; and December 2016, n=4. IAV, influenza A virus.

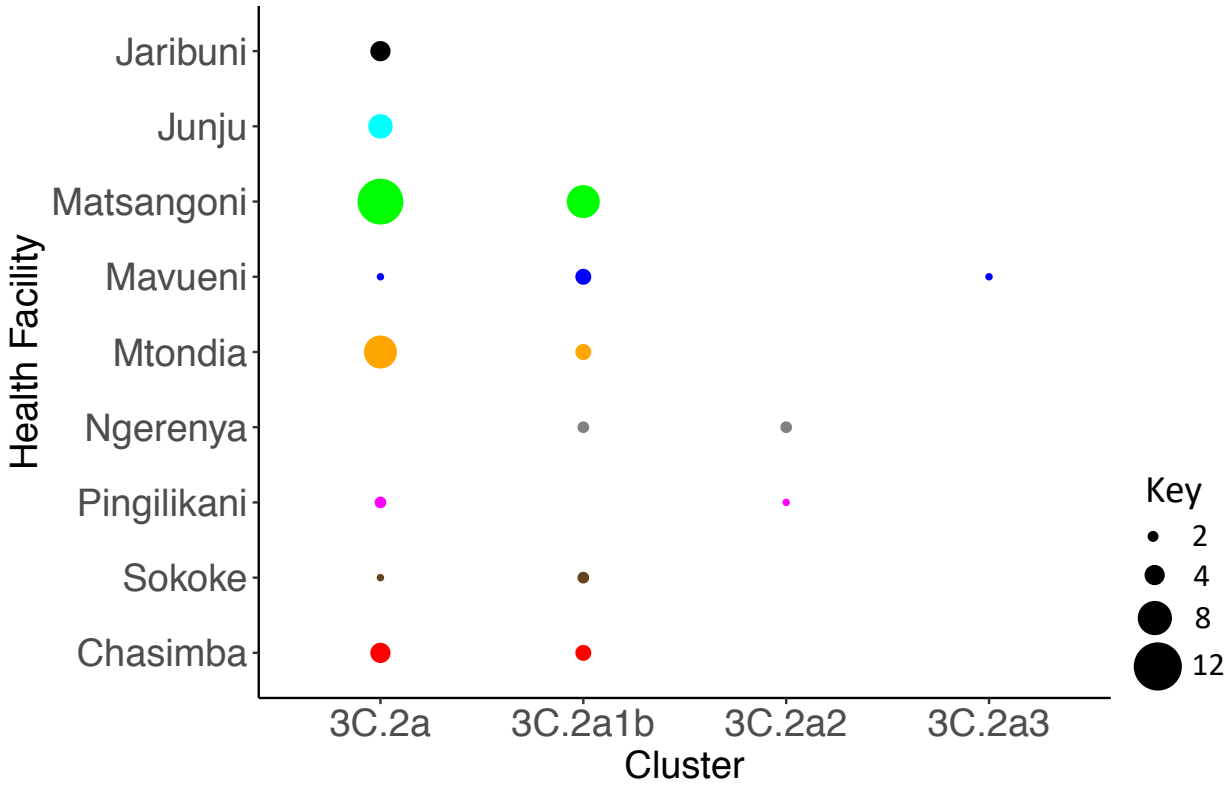


Figure 3.3: Bubble plot showing A(H3N2) virus genetic groups distributed by health facility. The distribution of the genetic groups was as follows: clade 3C.2a (n=34, 58.6%); subclades 3C.2a2 (n=3, 5.2%) and 3C.2a3 (n=1, 1.7%); and subgroup 3C.2a1b (n=20, 34.5%).

3.3.3 Reassortment Analysis

Tanglegrams were reconstructed for multiple pairs of all Kilifi A(H3N2) virus gene segment phylogenies to visualize similarities and differences between the phylogenetic tree pairs and detect reassortment events. The two phylogenetic tree pairs were visualized as time-resolved trees in a side-by-side conformation and connection lines between taxa that correspond to each other in the two trees were drawn to visualize similarities and differences in placement of viruses in the trees. One tree in the tanglegram pairs was based on HA phylogeny, which is used to characterize A(H3N2) virus strains into genetic groups, and whose topology is used to map phylogenetic leaf nodes. Visual inspection of all the tanglegram pairs revealed no evidence of reassortment, *Figure 3.4*. The concatenated whole-genome phylogenetic tree revealed a topology that was consistent with those generated using individual gene segments in the tanglegrams, with the four genetic groups corresponding to genetic groups inferred using HA characterization, *Figure 3.5*. These findings were verified computationally using the GiRaF reassortment analysis tool, which showed no evidence of reassortment in any of the eight A(H3N2) virus gene segments.

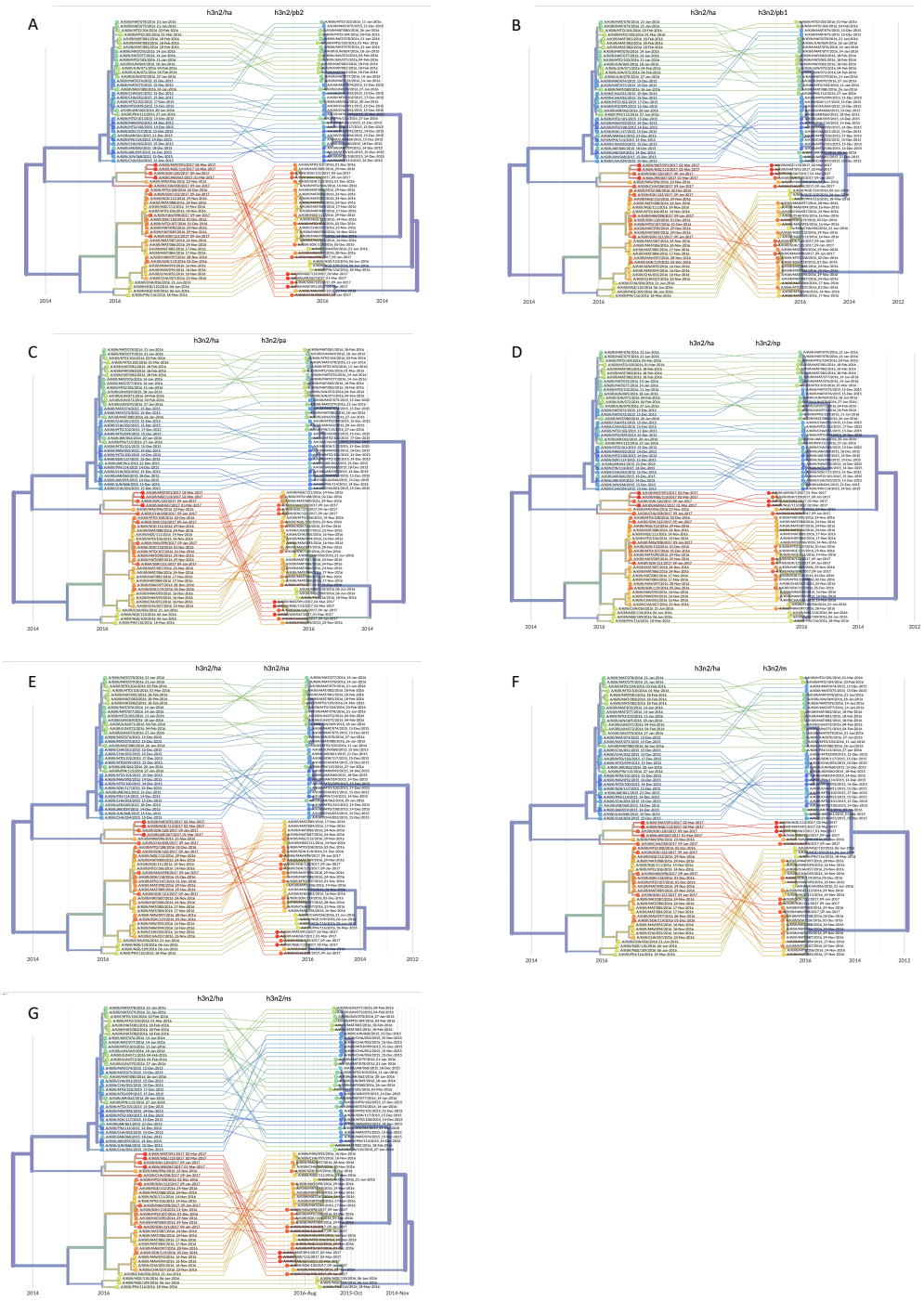


Figure 3.4: Influenza A(H3N2) virus gene segment tanglegrams for viruses from Kilifi reconstructed by maximum-likelihood methods for detection of reassortment events. The tanglegram pairs are as follows: panel (A), HA and PB2; panel (B), HA and PB1; panel (C), HA and PA; panel (D), HA and NP; panel (E), HA and NA; panel (F), HA and M; and panel (G), HA and NS.

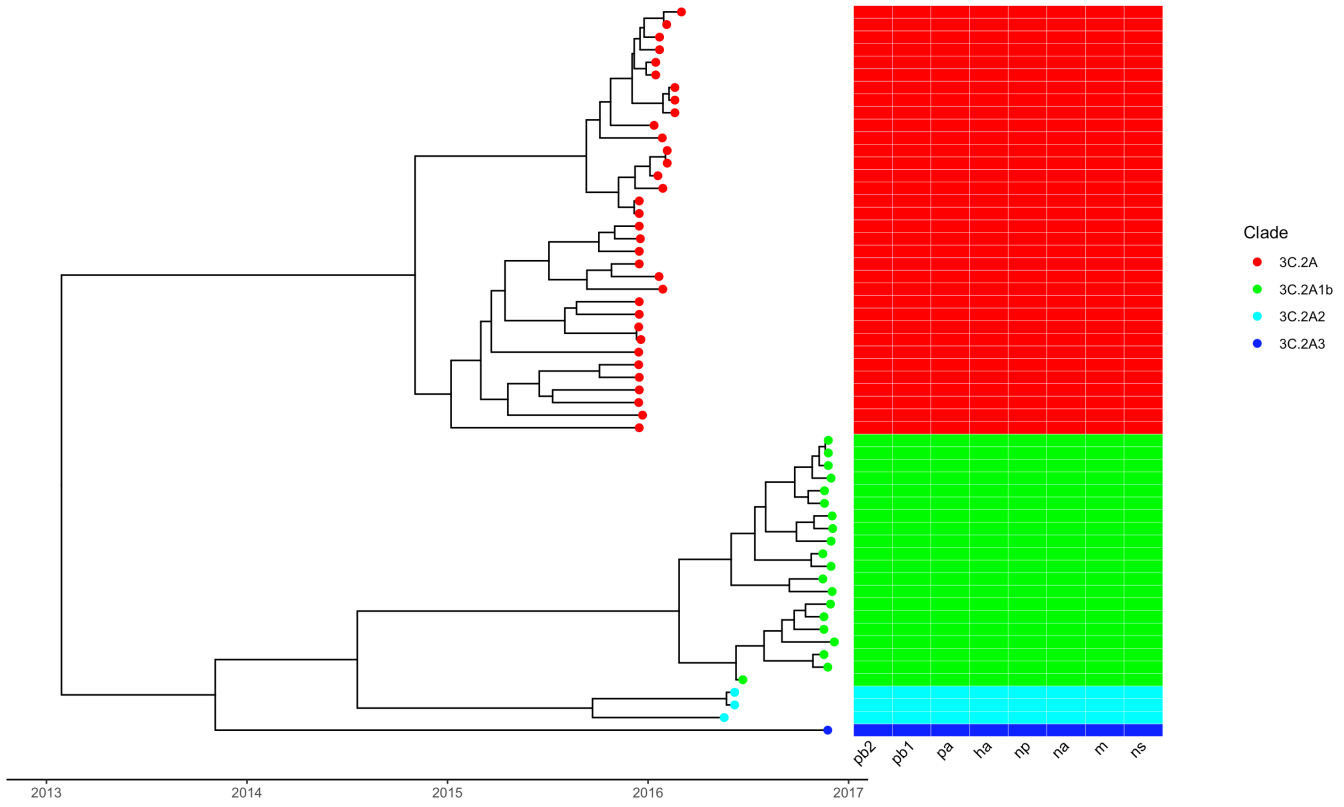


Figure 3.5: Phylogenetic tree of concatenated segments of A(H3N2) viruses from Kilifi, Kenya and schematic showing individual gene segment lineages. The time-resolved tree was constructed using 58 whole-genome sequences of A(H3N2) viruses by concatenating all the eight genome segments. Tips are colored by genetic group as follows: 3C.2a in red, 3C.2a1b in green, 3C.2a2 in cyan, and 3C.2a3 in blue. To the right is a schematic representation of viral clustering of each gene segment, which shows consistent lineage classification for all eight segments for all viruses.

3.3.4 Estimation of the Number of A(H3N2) Virus Introductions into Kilifi, Kenya

Ancestral state reconstruction using time-resolved phylogenies of A(H3N2) viruses from Kilifi and other global locations allowed identification of virus introductions into Kilifi, Kenya, which was based on 2 discrete location states that represent transitions from non-Kilifi to Kilifi states. Kilifi-specific transmission chains were identified using 3 criteria: (i) the cluster must be significantly supported with a phylogenetic bootstrap of >80%; (ii) the cluster must contain more than 2 isolates; and (iii) more than 80% of isolates within the cluster must be sampled within Kilifi, *Figure 3.6*. By this criteria, 3 Kilifi A(H3N2) virus clusters were identified, each consisting of 3 to 34 isolates, which represent at least 3 independent A(H3N2) virus introductions into Kilifi, Kenya during 2015-16 season. The clusters were assigned as KLF-1, KLF-2, and KLF-3 clusters, which also represent viruses within Kilifi clade 3C.2a (n=34), subgroup 3C.2a1b (n=20), and subclade 3C.2a2 (n=3), respectively. The estimated dates of introduction of these virus clusters, inferred from corresponding internal nodes of the global time-resolved phylogeny, were as follows: KLF-1, 12 January 2013; KLF-2, 26 June 2014; and KLF-3, 02 May 2014.

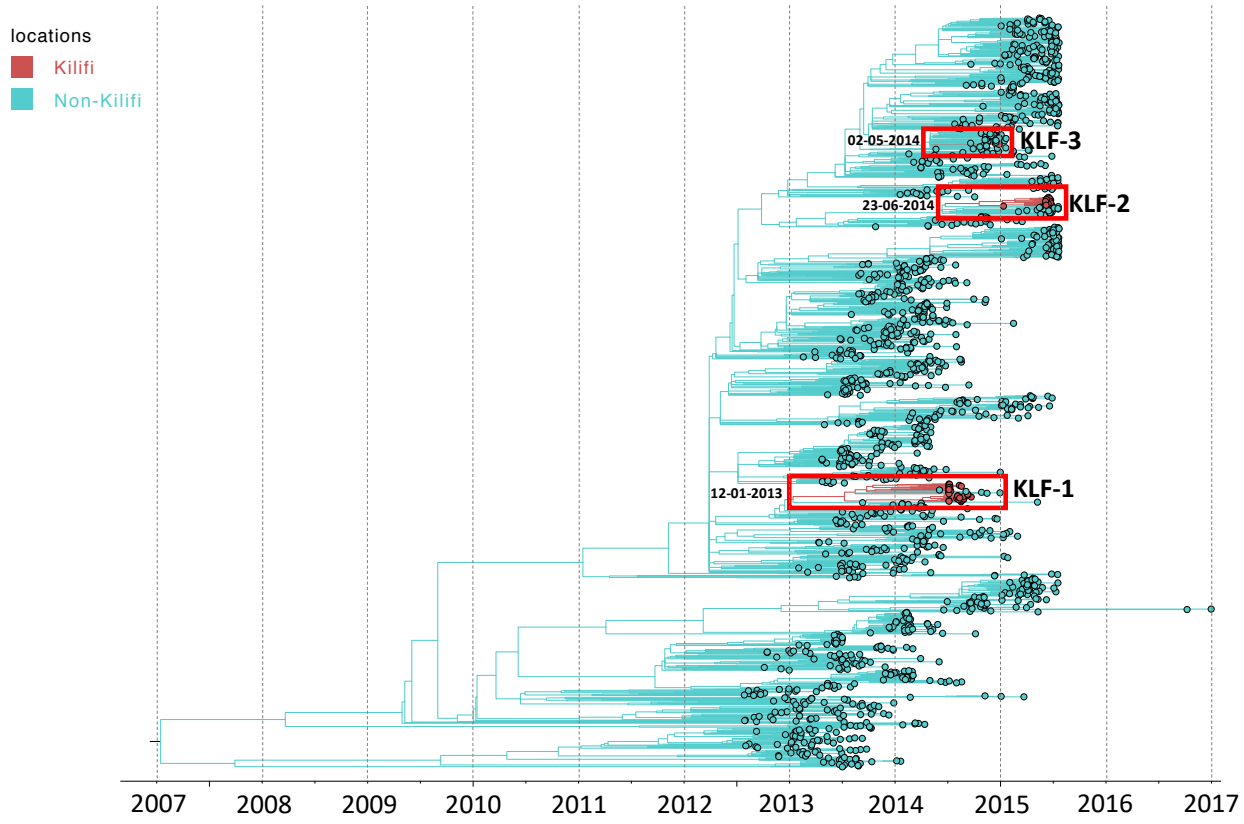


Figure 3.6: Time-resolved maximum-likelihood phylogenetic tree of Kilifi and contemporaneous global WGS data collected between 2014 and 2016. Unique Kilifi clusters are labelled with the prefix KLF: KLF-1, KLF-2, and KLF-3 (labelled using red boxes). The Kilifi clusters are shown for all the genetic groups identified in Kilifi during the 2015-2016 influenza season and provides evidence for multiple introductions of A(H3N2) viruses into Kilifi, Kenya during the study period, whose time to the most recent common ancestor are shown in calendar month inferred from corresponding internal nodes of the tree.

3.3.5 Global Phylogeny of A(H3N2) Virus Strains from Kilifi, Kenya

Additional analyses sought to identify the global sources of virus introductions into Kilifi, Kenya through reconstruction of global phylogenies of the 58 WGS data for viruses from Kilifi and 1,571 globally distributed WGS data, which revealed extensive global mixing of A(H3N2) viruses, *Figure 3.7* (hemisphere resolution) and *Figure 3.8* (continent resolution). The phylogeny showed extensive global mixing of A(H3N2) viruses, with co-circulation of virus lineages from Kilifi, Kenya with those from northern and southern hemisphere regions, including in countries in Africa, Asia, Europe, Oceania, South America, and North America. The clustering of A(H3N2) viruses from Kilifi with those from the 2 hemisphere regions suggest important roles of both hemispheres in seeding A(H3N2) viruses into Kilifi, Kenya. The viruses from each of the studied locations formed strongly supported clades with sequences for viruses from other regions (bootstrap values were usually >80%), which reflects a good phylogenetic resolution in the data. Much better supported clusters containing A(H3N2) viruses from Kilifi only were also observed (*Figure 3.7* and *Figure 3.8*).

Closer examination of the phylogenies of sequences from Africa provided evidence for the presence of strongly supported sub-lineages consisting predominantly of strains from Kilifi but also containing strains from elsewhere in Kenya, Uganda and Tanzania, for example, viruses clustering with Kilifi cluster KLF-1 (*Figure 3.9*). The finding of virus clusters consisting predominantly of strains from Kilifi and other strains from Kenya, Uganda and Tanzania is indicative of virus migration between these border-sharing countries. Additionally, strains from Kilifi fell into some strongly supported multinational sub-lineages consisting of strains from eastern Africa (Tanzania), central Africa (Rwanda and Congo), and southern Africa (South Africa,

Mozambique, Madagascar and Mayotte), for example, viruses clustering with KLF-3 cluster, which suggests possible migration of A(H3N2) viruses throughout Africa (*Figure 3.9*).

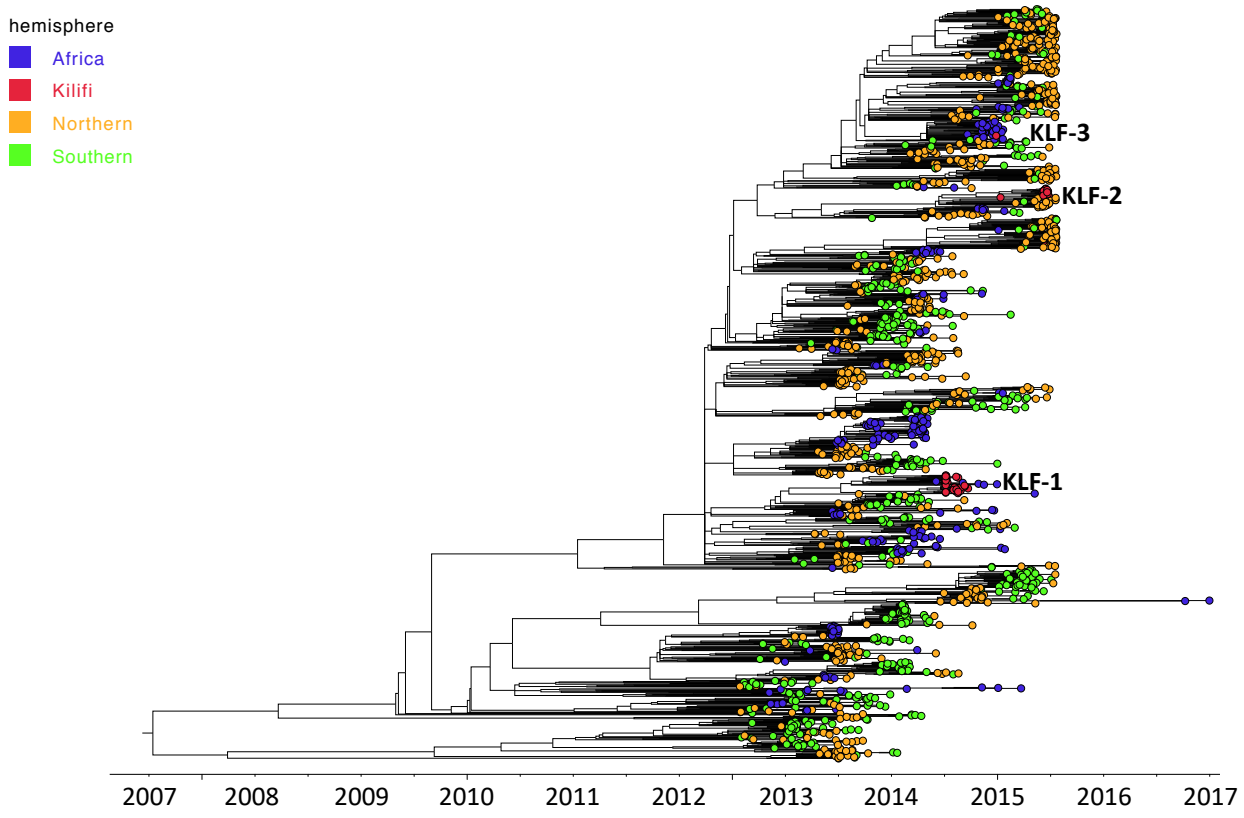


Figure 3.7: Time-resolved maximum-likelihood phylogeny of influenza A(H3N2) virus whole-genome sequences from Kilifi, Kenya and other global locations showing Kilifi, Africa, and the southern and northern hemisphere countries. The location Kilifi clusters, identified through ancestral state reconstruction (KLF-1, KLF-2, and KLF-3), are also shown in the global phylogeny.

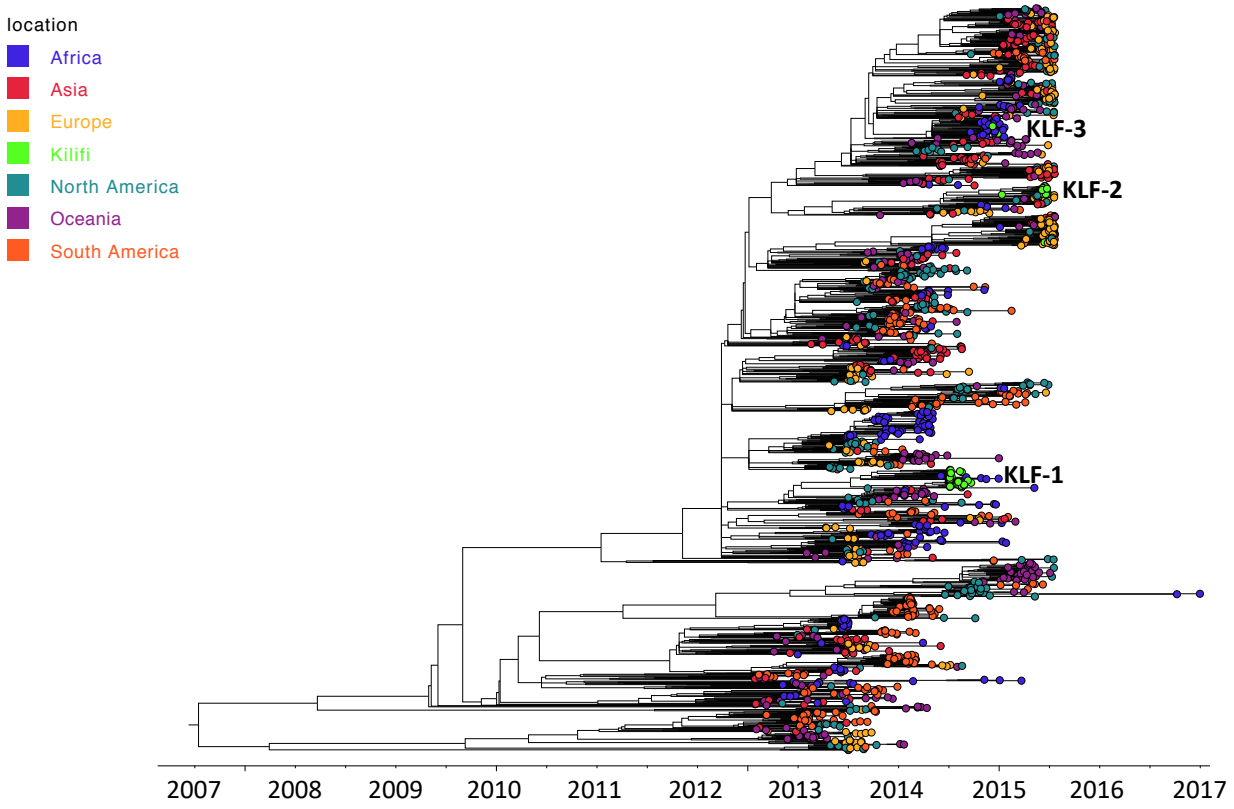


Figure 3.8: Time-resolved maximum-likelihood phylogeny of influenza A(H3N2) virus whole-genome sequences from Kilifi, Kenya and other global locations showing Kilifi and the continents of Africa, Asia, Europe, North America, South America, and Oceania. The location Kilifi clusters, identified through ancestral state reconstruction (KLF-1, KLF-2, and KLF-3), are also shown in the global phylogeny.

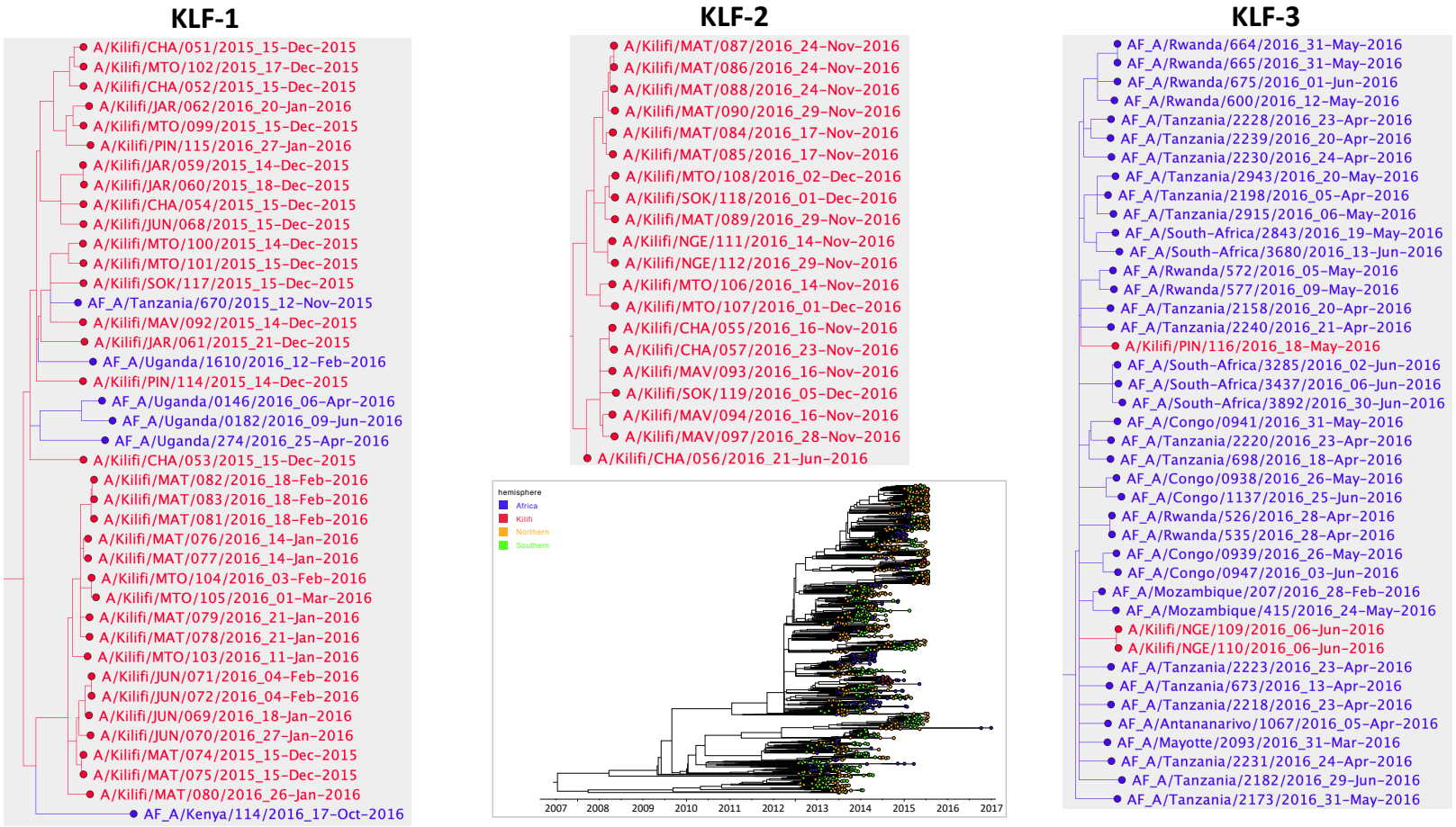


Figure 3.9: Time-resolved maximum-likelihood phylogeny of influenza A(H3N2) virus whole-genome sequences from Kilifi, Kenya and other global locations showing exploded views of clusters consisting of A(H3N2) virus clusters from Kilifi (KLF-1, KLF-2, and KLF-3). The figure shows: (i) clustering of Kilifi cluster KLF-1 viruses with viruses from Kenya and other East African countries; (ii) unique clustering of Kilifi KLF-2 viruses only; and (iii) clustering of Kilifi cluster KLF-3 viruses with those from the rest of the African continent.

3.3.6 Local Spread of A(H3N2) Virus in Kilifi, Kenya

The phylogeography of A(H3N2) virus in Kilifi, Kenya was reconstructed using BSSVS models to capture the underlying spatial migration dynamics of the virus among a set of 9 geographical locations (Chasimba, Jaribuni, Junju, Matsangoni, Mavueni, Mtondia, Ngerenya, Pingilikani and Sokoke); *Table 3.2* and *Figure 3.10*. Significant migration rates were observed from more populous locations to less populous locations, for example, from Chasimba (0.93-1.02) into Junju, Matsangoni, and Ngerenya and from Junju (0.92-0.96) into Mavueni, Mtondia, Pingilikani and Sokoke; *Table 3.2*. Significant migration rates were also observed between more populous locations, for example, from Junju to Mavueni and vice versa, *Figure 3.10*. Supported migration pathways were also observed for locations in proximity, for example, Pingilikani and Junju, and Mavueni and Jaribuni. The location estimates obtained by discrete phylogeographic reconstruction also revealed a strongly spatially structured A(H3N2) virus population in Kilifi, Kenya (*Figure 3.11*). The spatial structure is evident from clustering of viruses by KHDSS location, for example, in Matsangoni, Mavueni, and Junju, as shown in the time-resolved phylogeny (*Figure 3.11*).

The genetic relatedness of the Kilifi virus clusters by location is shown in *Figure 3.12*. In some of the facilities, it was clear that a dominant transmission cluster existed, for example, in Matsangoni and Junju for KLF-1 cluster viruses and Matsangoni and Mavueni for KLF-2 cluster viruses while some had no clear dominant transmission cluster. Here, the dominance of the transmission clusters in Matsangoni corroborates the strong spatial clustering structure observed for A(H3N2) virus in this location.

Table 3.2: Asymmetrical migration rates between location states in Kilifi inferred using the BSSVS model for influenza A(H3N2) virus.

	Migration rates*								
†	Chasimba	Jaribuni	Junju	Matsangoni	Mavueni	Mtondia	Ngerenya	Pingilikani	Sokoke
Chasimba	—	1.04	**0.93**	**1.02**	1.22	1.27	**0.95**	1.02	1.01
Jaribuni	1.01	—	0.96	0.97	0.95	0.98	0.95	0.99	0.97
Junju	0.96	0.95	—	0.98	**0.92**	**0.96**	0.96	**0.95**	**0.95**
Matsangoni	0.96	0.97	0.84	—	0.99	1.93	0.85	0.97	0.96
Mavueni	0.94	**0.97**	**0.95**	0.94	—	0.96	0.96	**0.96**	0.98
Mtondia	1.56	1.13	0.95	1.06	1.04	—	0.96	1.03	1.16
Ngerenya	0.96	0.95	0.96	0.96	0.94	0.93	—	0.94	0.96
Pingilikani	0.99	0.96	0.94	0.96	0.95	0.95	0.97	—	0.92
Sokoke	0.95	0.95	0.93	0.96	1.05	0.96	0.96	0.96	—

*Migration rates in bold indicate supported rates with Bayes factor ≥3.

†Number of sequences: Chasimba, 7; Jaribuni, 4; Junju, 5, Matsangoni, 17; Mavueni, 5, Mtondia, 10; Ngerenya, 4; Pingilikani, 3; and Sokoke, 3.

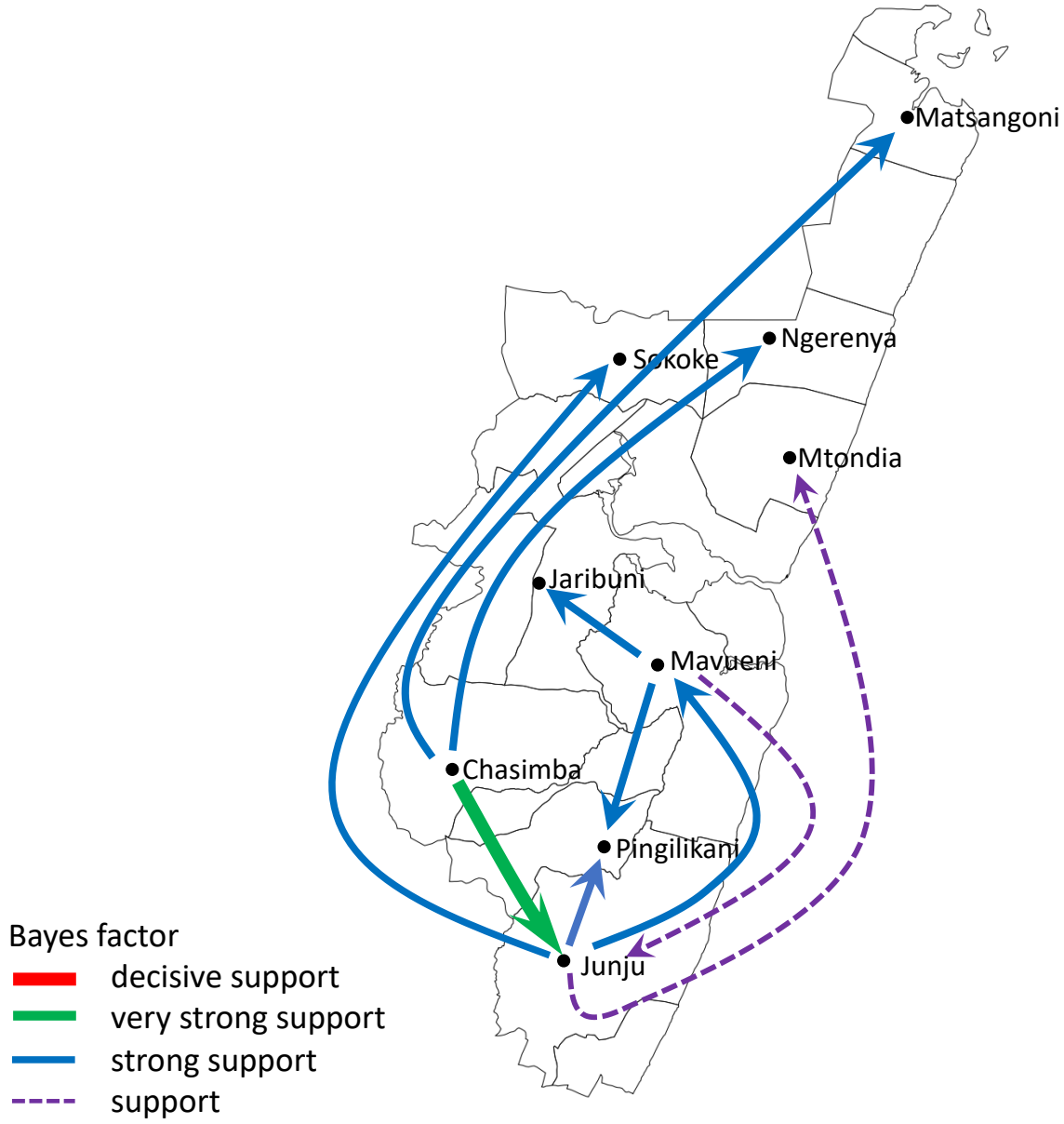


Figure 3.10: Migration networks of A(H3N2) virus reconstructed using sequence data from Kilifi, Kenya, 2015-16. Asymmetric migration pathways between location states were inferred for Kilifi locations. Coloured line arrows indicate significant migration routes from one location state to another, while line thickness represents the degree of statistical support. Red arrowed lines are shown to indicate decisive migration routes with Bayes factor (BF) support ≥1000; green lines represent very strongly supported routes with 100≤BF<1000; blue lines indicate strongly supported routes 10≤BF<100; and purple dotted lines indicate supported routes with 3≤BF<10.

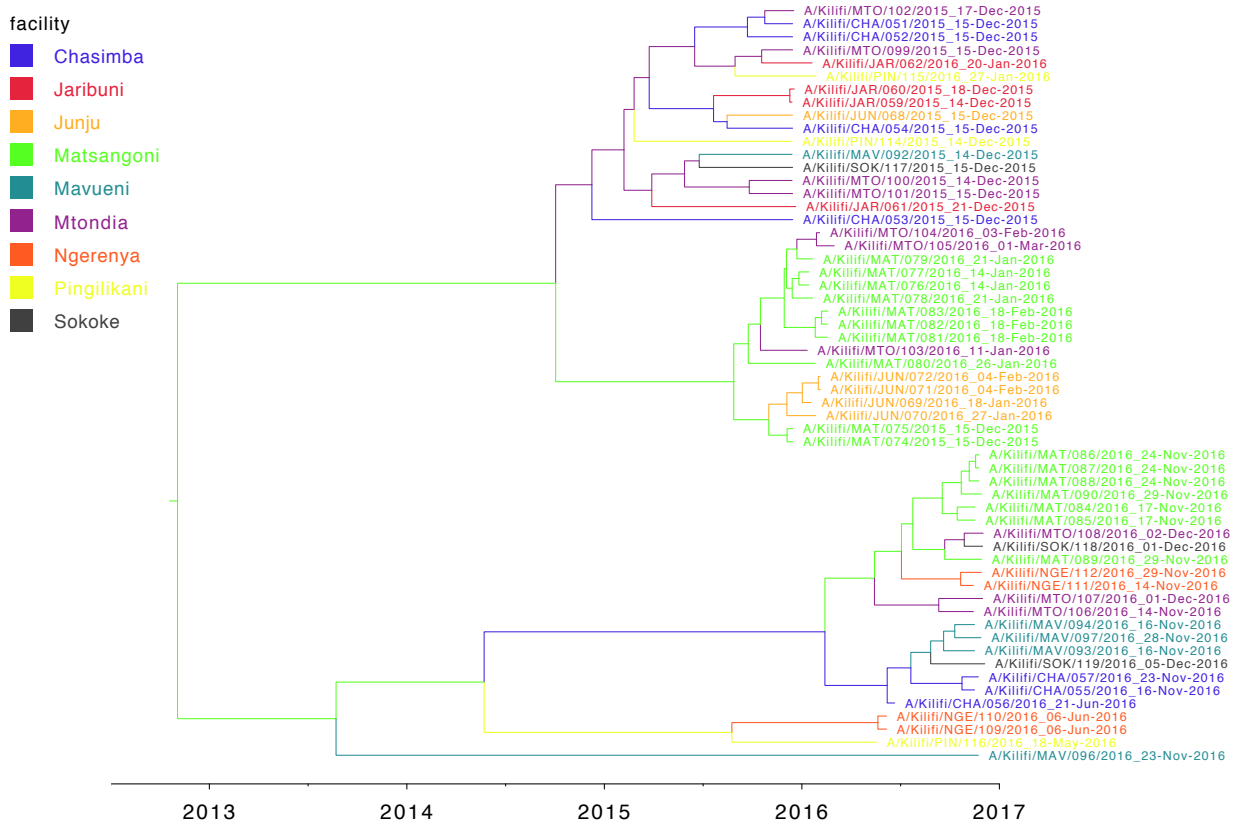


Figure 3.11: Time-resolved MCC tree inferred for A(H3N2) virus sequences from Kilifi, Kenya. Branches are coloured according to the most probable location state, which is indicated in the coloured key at the top left. MCC, maximum clade credibility.

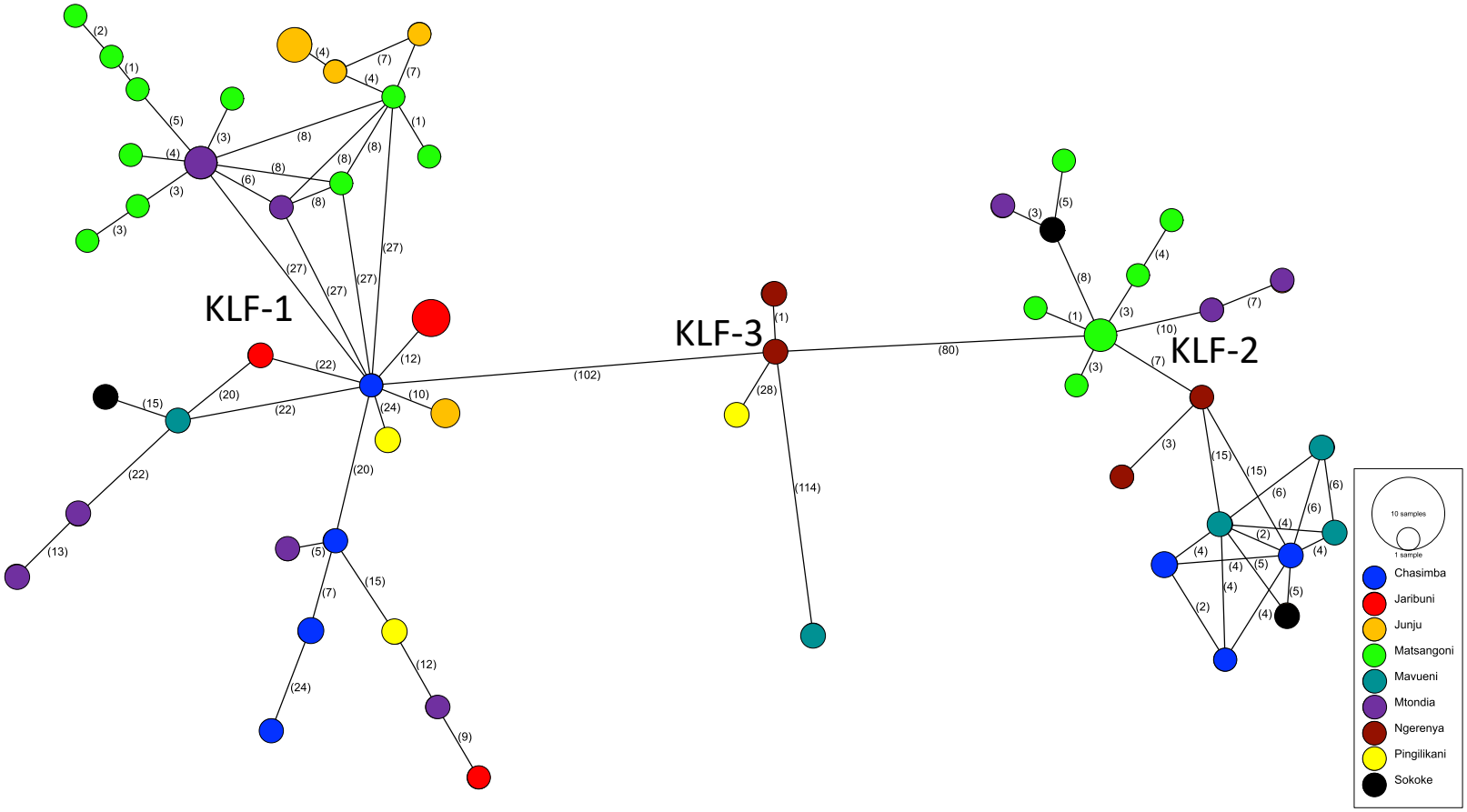


Figure 3.12: Possible transmission links between A(H3N2) viruses from Kilifi, Kenya. The figure shows a TCS PopART network of 58 newly sequenced A(H3N2) viruses. The vertices represent the concatenated genome haplotypes. The size of the vertex is proportional to the number of haplotypes (identical sequences) and is coloured by the health facility from which the sequenced sample was collected. The numbers shown on the edges represent the number of nucleotide changes from one vertex (haplotype) to the next.

3.3.7 Phylogeographic Structure of A(H3N2) Virus in Kilifi, Kenya

To determine the phylogeographic structure in the Kilifi WGS data using a statistical approach, phylogeny-trait association tests were conducted to determine phylogenetic association with sampling location (health facility) (*Table 3.3*). For strains from Kilifi, the results confirmed a stronger spatial clustering of sequences at all locations ($p<0.001$), which is also evident in the time-resolved tree (*Figure 3.11*). Additionally, the maximum clade statistic was significant ($p\leq0.05$) in most locations (6 out of 9) reflecting predominantly local evolution in most locations. The estimated differences in observed and expected maximum clade values tentatively suggested that Pingilikani and Sokoke exhibited the least spatial structure (i.e., most mixing; difference <0) while Matsangoni exhibited the strongest spatial structure (difference of 4), which statistically corroborates the observations from the time-resolved phylogeny (*Figure 3.11*) and transmission network (*Figure 3.12*) in which Matsangoni exhibited the strongest spatial structure in comparison to other locations in Kilifi, Kenya.

Table 3.3: Bayesian Tip-association Significance results.

Location	Association index (95% CI)			Parsimony scores (95% CI)			Mean maximum clade size (95% CI)			
	Observed	Expected	p values	Observed	Expected	p values	Observed	Expected	p values	Difference #
All	2.04 (1.77-2.32)	5.78 (5.07-6.45)	<0.001	25.65 (25-26)	37.59 (34.99-39.95)	<0.001	–	–	–	–
Chasimba	–	–	–	–	–	–	2.00 (2.00-2.00)	1.21 (1.00-1.99)	0.029	0.79
Jaribuni	–	–	–	–	–	–	1.99 (2.00-2.00)	1.06 (1.00-1.97)	0.004	0.93
Junju	–	–	–	–	–	–	3.99 (4.00-4.00)	1.13 (1.00-1.99)	0.009	2.86
Matsangoni	–	–	–	–	–	–	6.05 (6.00-7.00)	2.07 (1.01-3.05)	0.002	3.98
Mavueni	–	–	–	–	–	–	2.17 (2.00-3.00)	1.10 (1.00-1.99)	0.012	1.07
Mtondia	–	–	–	–	–	–	1.99 (2.00-2.00)	1.46 (1.00-2.23)	0.111	0.53
Ngerenya	–	–	–	–	–	–	1.99 (2.00-2.00)	1.08 (1.00-1.99)	0.005	0.91
Pingilikani	–	–	–	–	–	–	1.00 (1.00-1.00)	1.04 (1.00-1.01)	>0.999	-0.04
Sokoke	–	–	–	–	–	–	1.00 (1.00-1.00)	1.04 (1.00-1.15)	>0.999	-0.04

Abbreviations: CI, confidence interval.

3.4 Discussion

Relatively little is known about the role that tropical and sub-tropical African countries play in the global migration dynamics of influenza viruses due to insufficient spatiotemporally representative sequence data from the region (Ng and Gordon, 2015; Viboud et al., 2013). This is despite the region bearing a disproportionately large burden of influenza (Gessner et al., 2011; Katz et al., 2012b). Here, through a comprehensive genomic analysis, it is shown that the year-round circulation of A(H3N2) virus in a coastal Kenya region was characterized by the co-circulation of multiple virus genetic groups and clusters. Additionally, it is revealed that the epidemic season was instigated by at least 3 independent virus introductions into Kilifi, Kenya detected out of 58 sequenced samples collected between December 2015 and December 2016. The genomic analysis revealed extensive local spread of new virus strains throughout Kilifi once introduced, which was associated with predominantly local evolution in most of the locations in Kilifi.

Phylogenetic analysis revealed multiple A(H3N2) virus introductions, each introduction commonly circulating in multiple study locations in a relatively short period of time. However, the small sample size may have limited the spatiotemporal inference of viral introductions into Kilifi. Following virus introduction, local virus spread in Kilifi was predominantly characterized by virus spread from more populous to less populous locations and between more populous locations. Additionally, locations in proximity also had well supported migration pathways. The spread of A(H3N2) virus from the populous to less populous locations has been reported in other tropical regions (Pollett et al., 2015). There was strong spatial clustering of A(H3N2) viruses in majority of the locations, which is consistent with semi-localized virus epidemics in Kilifi although with migration between localities. Such semi-localized A(H3N2) virus epidemics have been reported elsewhere (Nelson et al., 2006; Pollett et al., 2015). The strongest spatial structure was observed

in the most populous locations, for example, in Matsangoni, which was associated with rapid and widespread virus spread; weaker spatial clustering in the less populous locations was likely associated with limited virus spread. Additionally, the dominance of virus transmission clusters confirmed existence of a strong spatial structure in the most populous locations, for example, in Matsangoni with this structure associated with predominantly local evolution in the studied locations.

Phylogenetic analysis revealed an extensive global migration of A(H3N2) viruses and that mixing of viruses from Kilifi, Kenya with those from multiple global regions was widespread, evident from the local and global phylogenies (hemisphere and continent phylogenies) in which Kilifi sequences span the global diversity, suggesting strong exchange of viruses from Kilifi with other areas around the world. These findings are consistent with those of studies from other countries, which showed regular introductions of new A(H3N2) virus lineages and seeding of local seasonal epidemics (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Russell et al., 2008) rather than inter-seasonal persistence of virus lineages (Holmes et al., 2005; Nelson et al., 2007; Nelson et al., 2006; Russell et al., 2008). For example, annual epidemics in Australia and USA are associated with multiple introductions of influenza viruses that then establish transmission chains across the country (Geoghegan et al., 2018; Nelson et al., 2008). Notably, there was evidence of migration of A(H3N2) viruses between Kilifi, Kenya and its neighbor countries in East Africa, although this conclusion was uncertain due to small number of sequences from these countries. Both the northern and southern hemispheres were predicted to be source populations for introductions of A(H3N2) viruses into Kilifi, Kenya, which supports the model of global migration of influenza viruses (Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2014; Russell et al., 2008).

The observation that viruses from Kilifi clustered with those from both hemispheres suggest that introductions of A(H3N2) viruses into Kilifi originate from the two hemispheres without predominance of any hemisphere. Rapid global movement of people, especially through air travel, plays an important role in the global circulation dynamics of influenza viruses (Lemey et al., 2014). For example, Europe as a potential source of introductions of A(H3N2) viruses into Kenya or a destination for viruses from Kilifi, Kenya is evident from the fact that Europe accounts for the largest single group of tourists to Kenya (Oxford Business Group, 2017) with coastal Kenya being a major tourist hub in the country. Additionally, the influx of people from Asia is based on the increasing Chinese economic interests in Africa (including Kenya), which has resulted in an increased influx of Chinese into Africa for trade, work and tourism (Economist, 2013). Viruses from Kilifi, Kenya also fell into some strongly supported multinational sub-lineages consisting of strains from central and southern African countries, which suggests considerable virus migration throughout the continent. However, there were fewer WGS data of A(H3N2) viruses from Africa during the study period to examine intra-African transmission dynamics in detail.

Following introduction and circulation, A(H3N2) virus strains regularly underwent extinction, which suggests that much of the genetic diversity of viruses in Kilifi results from global lineages of A(H3N2) viruses that migrate through Kilifi, Kenya rather than from local evolution associated with long-term local persistence. However, the small sample size may have limited the inference of local virus extinction. These findings are consistent with those of studies from other countries in which the genetic diversity of seasonal influenza viruses in specific locales primarily results from the ongoing introduction of genetically divergent IAV lineages during seasonal epidemics (Holmes et al., 2005; Nelson et al., 2007; Rambaut et al., 2008). In contrast, inter-seasonal persistence of A(H3N2) viruses has been documented in tropical and sub-tropical regions like

Hong Kong and Southeast Asia (Bahl et al., 2011; Le et al., 2013; Tang et al., 2008) whereas multi-year persistence of A(H1N1)pdm09 virus strains in tropical areas of western Africa, which are relatively isolated, has also been shown (Nelson et al., 2014).

That the findings from this study are not consistent with the circulation patterns of influenza viruses described in tropical and sub-tropical countries, where inter-seasonal persistence of influenza has been shown, suggests that the migration dynamics in tropical and sub-tropical regions are far more complex than those represented by existing models of IAV circulation. Rather the findings are consistent with the shifting metapopulation model of circulation of A(H3N2) viruses (Bahl et al., 2011) in which viruses may pass through any region for a variable amount of time rather than perpetually circulating in fixed locations in the tropics and consistently seed temperate regions each year (Lemey et al., 2014; Russell et al., 2008). Such a shifting metapopulation model may explain why some studies show apparent persistence in some tropical and sub-tropical regions over certain years whereas others, like Kilifi, do not (Bahl et al., 2011; Cheng et al., 2013; Le et al., 2013; Nelson et al., 2014).

These findings have implications for public health practice in Kilifi and the rest of the country. The rapid spread of A(H3N2) viruses throughout Kilifi, considering it being a remote rural region, provides evidence of how quickly IAV can disseminate once introduced into a country. There was evidence that the most populous locations in Kilifi, Kenya are possible hubs for spread of influenza viruses; perhaps these could be prioritized for heightened surveillance should a novel influenza subtype be introduced in the local community. Lastly, the rapid and widespread migration of global strains into Kilifi, Kenya and widespread global mixing with influenza viruses from both hemispheres emphasize that vaccine recommendations in either hemispheres need well distributed, widespread global sampling of A(H3N2) viruses from as many localities as possible.

CHAPTER FOUR

4 Phylogeography of Influenza A(H1N1)pdm09 Virus in Kenya, 2009-2018

4.1 Introduction

A novel influenza A(H1N1)pdm09 virus emerged in the Americas during March-April 2009, spread rapidly among humans, and developed into the first human pandemic of the 21st century (CDC, 2009; Dawood et al., 2009; Garten et al., 2009; Smith et al., 2009). The initial pandemic period was characterized by rapid transmission and spread of the virus, with 168 countries reporting infections by July 2009, which was associated with 162,300 laboratory-confirmed cases and over 1,100 human deaths (Holmes et al., 2011; Nelson et al., 2009; Rambaut and Holmes, 2009). Subsequently, it was estimated that 201,200 respiratory deaths (range 105,700-395,600) and an additional 83,300 cardiovascular deaths (range 46,000-179,900) were associated with the pandemic; 80% of the respiratory and cardiovascular deaths occurred in people aged ≤65 years, with 51% of these deaths occurring in southeast Asia and Africa (Dawood et al., 2012). A(H1N1)pdm09 virus has subsequently caused seasonal epidemics following the pandemic period, and continues to co-circulate with influenza A(H3N2) and influenza B viruses in all countries (Baillie et al., 2012; Nelson et al., 2011; Venter et al., 2012; Zehender et al., 2012) including Kenya (Emukule et al., 2014; Emukule et al., 2019; Katz et al., 2012a; Katz et al., 2014; Onyango et al., 2012a). The emergence of A(H1N1)pdm09 virus resulted in the rapid replacement of seasonal A(H1N1) virus that had circulated in humans for over 32 years from 1977 to 2009 (Kilbourne, 2006).

The 2009 influenza pandemic being the first to occur in the genomic era saw over 2,000 influenza virus genomes made publicly available from infections during 2009-10 alone (Su et al., 2015). Analysis of the viral genomes provided a unique opportunity to study the emergence and

establishment of a novel pathogen in humans across different spatiotemporal scales of observation particularly in regions with comprehensive influenza sentinel surveillance systems. As a consequence, the early spread and diversification of A(H1N1)pdm09 virus (Baillie et al., 2012; Lemey et al., 2009b; Nelson et al., 2009; Rambaut and Holmes, 2009) and its ongoing evolution and transmission (including genetic and antigenic drift, and global migration dynamics) were well described (Bedford et al., 2015; Lemey et al., 2014; Su et al., 2015). The genomic analyses revealed that distinct virus lineages arose early in the pandemic and rapidly disseminated globally (Garten et al., 2009; Nelson et al., 2009). However, the patterns of introduction and spread of A(H1N1)pdm09 virus in low- and middle-income countries, including its ongoing evolution have not been thoroughly investigated due to limited virus sequence data from these regions (Ng and Gordon, 2015; Venter et al., 2012; Viboud et al., 2013).

Analysis of viral WGS data is particularly important in defining the within-country evolution and spread of influenza viruses. For example, in the UK, the spread of A(H1N1)pdm09 virus was described, in which multiple independent introductions of genetically distinct viruses into the country was documented. Multiple strains co-circulated in the first pandemic wave, persisted into the second wave, and disseminated further as 2 transmission chains within the country (Baillie et al., 2012; Galiano et al., 2011). Similar observations were made in Scotland (Lycett et al., 2012), whereas in Italy strong founder effects following multiple virus introductions resulted in local amplification of infections in the second epidemic wave with isolates from the second wave exhibiting greater divergence from the first wave (Zehender et al., 2012). In the USA, clear spatial patterns were observed in the early stages of the pandemic in which strong founder effects resulted in genetically distinct viral clades sweeping through New York State and Wisconsin between April and May 2009. The spatial structure was subsequently disintegrated by extensive global mixing

during the second wave, which was dominated by a single clade that had been dominant in New York city in the first wave (Nelson et al., 2011). Taken together, such investigations led to the deduction that major epidemics of influenza virus are usually followed by deep troughs that are strongly driven by seasonal bottlenecks, multiple viral re-introductions into regions after the first wave, and sustained viral extinction between epidemics (Su et al., 2015; Viboud et al., 2013; Vijaykrishna et al., 2015). Additionally, there are complex spatiotemporal patterns of viral genetic diversity within specific localities, especially the presence of multiple co-circulating lineages, which require sufficient viral sampling depth to be described (Viboud et al., 2013). However, such spatiotemporal patterns of A(H1N1)pdm09 viruses have not been properly investigated in Africa (Viboud et al., 2013) with limited studies conducted in only 5 countries (Byarugaba et al., 2016; Dia et al., 2013; Gachara et al., 2016; Nelson et al., 2014; Venter et al., 2012).

In Kenya, influenza surveillance activities by the Kenyan Ministry of Public Health and Sanitation (MoPHS) reported 4 parallel introductions of A(H1N1)pdm09 virus into Kenya during the pandemic in 2009. The first laboratory-confirmed case of A(H1N1)pdm09 virus in Kenya was reported on June 29, 2009, in a traveler who had flown into Nairobi from London on June 21, 2009 then traveled to western Kenya by bus among a group of 34 travelers from the UK. The infection gave rise to 11 secondary laboratory-confirmed cases within the group (CDC, 2009a). A separate group of 4 travelers arrived in Nairobi from London and traveled to western Kenya by bus; 2 of the 4 travelers had laboratory-confirmed A(H1N1)pdm09 virus confirmations with evidence of secondary transmission from an index case in the UK. Two young boys who had flown from London to Kenya on vacation, in the company of 2 family members, were laboratory-confirmed as cases and were reported as the third known introduction of the virus into Kenya. The fourth introduction of the virus was by a returning Kenyan student from the UK who had reported contact

with an index case in the UK; this laboratory-confirmed secondary transmission resulted in 1 tertiary case in the student's household (CDC, 2009a). After the first case of A(H1N1)pdm09 virus was reported, the MoPHS conducted detailed contact tracing to identify additional laboratory-confirmed cases following these introductions and subsequent secondary and tertiary cases (CDC, 2009a; Osoro et al., 2011). The pandemic in Kenya was characterized by a single wave, which started in July 2009 and peaked in November 2009 (Osoro et al., 2011). Influenza A(H1N1)pdm09 virus vaccines became available in October in North America, Australia and Europe. In early 2010, the WHO began providing some developing countries with monovalent A(H1N1)pdm09 virus vaccines; Kenya received 730,000 doses in March 2010 (KNBS, 2010), which was prioritized for healthcare personnel, pregnant women and individuals with chronic illnesses (World Health Organization, 2009).

To investigate the evolution and transmission of influenza A(H1N1)pdm09 virus in Kenya, 383 A(H1N1)pdm09 virus WGS data sampled between 2009 and 2018 from 7 locations in Kenya along with 1,587 publicly available global WGS data were analyzed. Here, insights into the spatial and temporal evolutionary and migration dynamics of A(H1N1)pdm09 virus in Kenya since its introduction into the local population is presented, and its evolution and entrenchment as a human seasonal influenza virus in the same population is followed. These dynamics were investigated by comparing virus sequences in the pandemic (2009-10) and post-pandemic periods (2011 onwards) to describe the spatiotemporal evolutionary and migration dynamics of A(H1N1)pdm09 virus within Kenya in the past decade.

4.2 Methods

4.2.1 Local (Kenya) Sample Details and Sequencing

A total of 418 A(H1N1)pdm09 virus positive samples from CDC-Kenya collected from July 2009 to December 2018 in KNH, Nakuru County and Referral Hospital, Nyeri County and Referral Hospital, Kakamega County and Referral Hospital, Siaya County and Referral Hospital and Coast General Teaching and Referral Hospital (see Chapter Two, section 2.3.1 and 2.3.3 for an elaborate description of the studies and sample details) were available for this project. A further 45 A(H1N1)pdm09 virus positive samples collected from July 2009 to December 2018 from Kilifi County and Referral Hospital (see Chapter Two, section 2.3.2 for an elaborate description of the study and sample details) were included in the study. Initial sample screening for A(H1N1)pdm09 virus, nucleic acid extraction, IAV genome amplification, and IAV genome assembly was performed as described in the Chapter Two (sections 2.5.1, 2.5.2, 2.5.3, and 2.6.4).

4.2.2 Global Genome Sequence Dataset Collation

Global A(H1N1)pdm09 virus WGS data used in the analyses were all retrieved from the GISAID EpiFlu™ database (https://platform.gisaid.org/epi3/cfrontend) and processed as described in Chapter Two, section 2.7.2. A final dataset of 1,587 global sequences sampled from March 2009 to December 2018 was available (numbers in parenthesis indicate number of sequences): Africa (155); Asia (372); Europe (326); North America (356); South America (181); and Oceania (197).

4.2.3 Phylogenetic Analysis

Consensus nucleotide sequences were aligned and translated in AliView v1.26 (Larsson, 2014). The individual genome segments were concatenated into full-length genomes using SequenceMatrix (Vaidya et al., 2011). Phylogenetic trees based on WGS data of A(H1N1)pdm09

viruses from Kenya and contemporaneous global sequences were constructed with maximum-likelihood and bootstrap analysis of 1,000 replicates (to evaluate the robustness of the phylogenetic clustering). The best-fit nucleotide substitution models were inferred using IQ-TREE v1.6.11 (Kalyaanamoorthy et al., 2017; Nguyen et al., 2014) and those identified by the BIC for each concatenated virus genome implemented. The phylogenetic trees were visualized and annotated using Figtree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). The full-length HA sequences of all the virus genome sequences were used to characterize A(H1N1)pdm09 virus strains into genetic groups (i.e., clades, subclades, and subgroups) according to the European CDC Guidelines (https://www.ecdc.europa.eu/en/seasonal-influenza/surveillance-and-disease-data/influenza-virus-characterisation) and PhyCLIP (Han et al., 2019), which uses linear integer programming to assign sequences into genetic groups.

4.2.4 Discrete Phylogeographic Analysis and Ancestral State Reconstruction

All the Kenyan WGS data generated in this study were used to perform a discrete phylogeographic analysis whereas the combined Kenyan and contemporaneous global WGS data were used for ancestral state reconstruction of geographic region, which estimates geographic ancestry of viruses. The spatial patterns of virus spread among a set of 7 geographic locations in Kenya (Nairobi, Nakuru, Nyeri, Siaya, Kakamega, Mombasa, and Kilifi; see Chapter Two, *Figure 2.1*) were estimated using all the A(H1N1)pdm09 virus WGS data from Kenya generated in this study. Phylogeographical analysis was conducted to assess virus migration between these Kenyan locations using methods implemented in BEAST v1.10.4 package (Suchard et al., 2018). The analysis was implemented with an asymmetric discrete trait approach, which applied the BSSVS model (Lemey et al., 2009a). Phylogeographic inferences were visualized with the SPREAD3 v0.9.7.1c package (Bielejec et al., 2016). To visualize the geographic spread of the virus over time,

a D3 file was generated using SPREAD3 v0.9.7.1c package (Bielejec et al., 2016). A Kenya geo.json file was used for visualization and resulting log files were used to calculate BF values for significant migration rates between discrete locations. The MCMC chains were run until convergence, which was evaluated in Tracer software (Suchard et al., 2018) then TreeAnnotator (Suchard et al., 2018) was used to summarize the location estimates on MCC trees after discarding 10% of the trees as chain burn-in. The MCC trees with annotations were then visualized using Figtree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

Analysis of 405 Kenyan (383 A(H1N1)pdm09 virus WGS data and 22 additional Kenyan WGS data from GISAID) and 1,565 contemporaneous global WGS data from other countries would enable ancestral state reconstruction for the geographical region of internal nodes in TreeTime's time-resolved maximum-likelihood phylogenies using a discrete trait approach (Sagulenko et al., 2018). Two discrete states were selected for the global transition trait (i.e., Kenyan and non-Kenyan). From this analysis, specific internal nodes would be identified that represent virus introductions into Kenya (i.e., transitions from non-Kenyan to Kenyan states) in the time-resolved phylogenies. The estimated dates of introductions would be based on inferred dates of corresponding internal nodes, that is, internal nodes where transitions from non-Kenyan to Kenyan states were observed; inferred dates from internal nodes were then used to determine the number of virus introductions into Kenya throughout the study period and during the pandemic period 2009-10 in particular.

Analysis files and scripts can be found on GitHub: https://github.com/DCollinsOwuor/H1N1pdm09_virus_Kenya_phylogeography.

4.3 Results

4.3.1 IAV Whole-Genome Sequencing and Assembly

IAV positive samples were available from CDC-Kenya and KCH for this study, respectively. First, a total of 418 A(H1N1)pdm09 virus positive samples were available for this project from CDC-Kenya. Of these 418 positive samples, 414 (99%) that passed pre-sequencing quality control checks (see Chapter Two, section 2.5.3 for the quality control techniques for IAV amplicons and libraries) were loaded onto the Illumina MiSeq System, with subsequent success in generating 344 (83.1%) WGS and 66 (15.9%) partial A(H1N1)pdm09 virus genomes, respectively. For this report, only the 344 A(H1N1)pdm09 virus WGS data were used. Second, a total of 157 IAV positive specimens were available for this project from KCH. Of the 157 IAV samples, 94 (59.9%) that passed pre-sequencing quality control checks (see Chapter Two, section 2.5.3 for the quality control techniques for IAV amplicons and libraries) were loaded onto the Illumina MiSeq System with corresponding success in generating 45 (47.9%) (39 WGS and 6 partial) A(H1N1)pdm09 virus and 49 (52.1%) (46 WGS and 3 partial) A(H3N2) virus genomes, respectively. For this report, only the 39 A(H1N1)pdm09 virus WGS data were used. Phylogenetic analysis showed that the 383 A(H1N1)pdm09 virus WGS data (344 and 39 WGS from CDC-Kenya and KCH, respectively) comprised 7 genetic groups: clades 7 (n=97, 25.3%) and 6 (n=132, 34.5%); subclades 6C (n=10, 2.6%), 6B (n=47, 12.3%) and 6B.1 (n=38, 9.9%); and subgroups 6B.1A (n=57, 14.9%) and 6B.1A1 (n=2, 0.5%) as shown in *Appendix 7.2.1*. The GISAID accession numbers for the WGS data are also shown in the table.

Following MiSeq sequencing, a total of between 90,000 and 1,300,000 short reads were available per sample of which IAV-specific reads ranged between 1,000 to 1,200,000 reads (each of 250 bases) as shown in *Appendix 7.2.1*. All the genome assemblies were 13,133 nucleotides in length

with mean depth of base coverage per genome ranging from 19 to 22,800 (calculated from, for example, [1,200,000 reads X 250 bases]/13,133). With regards to sequence availability in GISAID, these are among the first geographically and temporally comprehensive representation of A(H1N1)pdm09 viruses generated from Kenya using high-throughput technologies within the country. Therefore, my project made an important contribution to the available sequence data from the country, which can be used to improve understanding of the phylogeography of IAV in Kenya, the African continent, and worldwide.

4.3.2 Spatiotemporal Representativeness of Sequenced Samples

Influenza A(H1N1)pdm09 virus was detected throughout the study period in Kenya with the number of observed cases fluctuating from year-to-year between 2009 and 2018, *Figure 4.1*. The different locations experienced peak prevalence in different years of the surveillance, but there was detection of the virus in all the surveillance sites, except in mid-2010, 2012-2013, and 2016 whereby most sites experienced limited virus detections. Of note is that Siaya sampling ended in 2013 while samples were only available from Mombasa in 2018. The proportion of samples from each surveillance site that were sequenced roughly reflected the overall distribution of positives that were detected in the specific surveillance sites, *Figure 4.1*. All the genetic groups of A(H1N1)pdm09 viruses were detected in most of the surveillance sites with the majority of the genetic groups detected in 5 or 6 of the 7 surveillance sites, which suggests that the lineages of A(H1N1)pdm09 viruses were in circulation throughout the country with limited geographical restrictions to particular viral lineages throughout the study period, *Figure 4.2*. The detections also varied by surveillance year: clade 7 – 2009-2012; clade 6 – 2009-2011; subclade 6C – 2013-2014; subclade 6B – 2014-2016; subgroup 6B.1 – 2015-2016; and subgroups 6B.1A and 6B.1A1 – 2018, *Figure 4.3*.

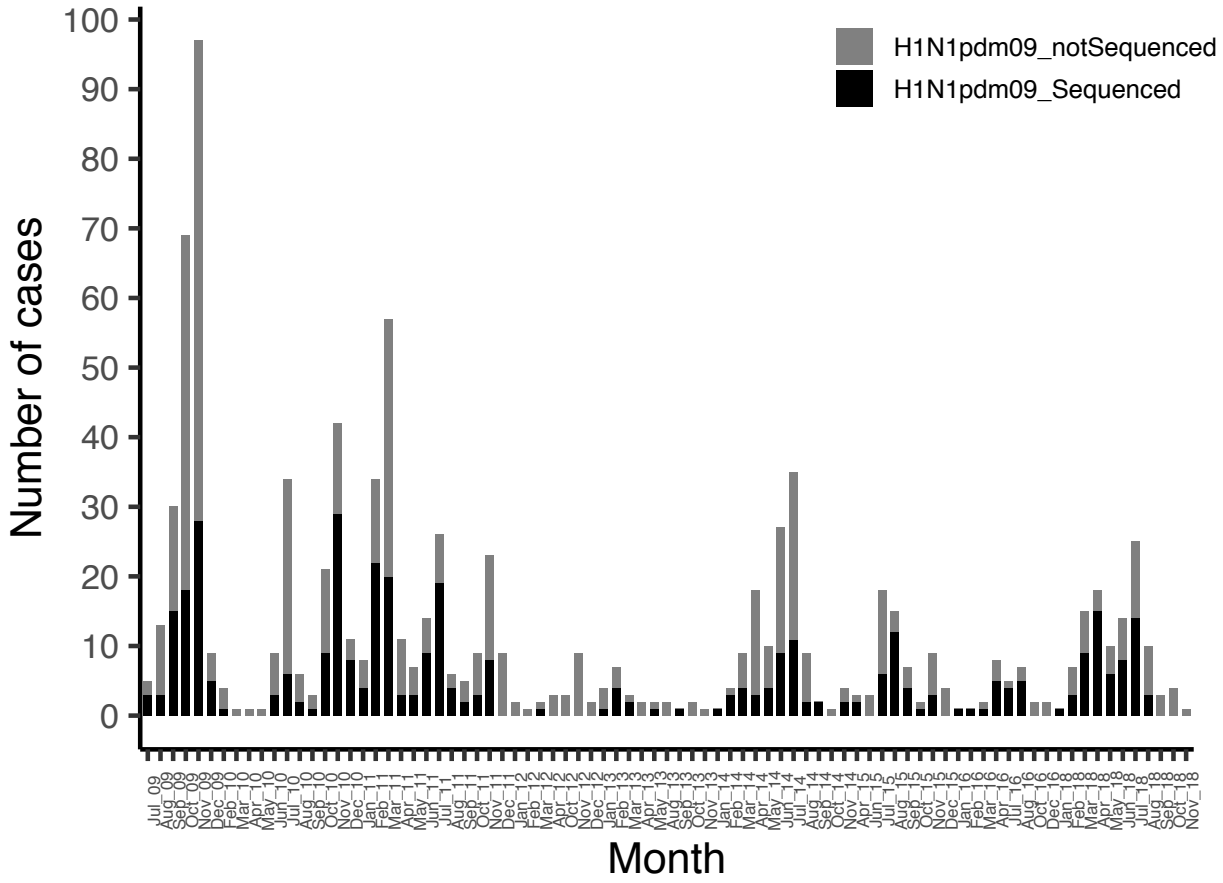


Figure 4.1: Bar plot showing number of A(H1N1)pdm09 virus positive samples and sequenced positive samples by month and surveillance site between July 2009 and November 2018 in Kenya. All collected A(H1N1)pdm09 virus positive samples and sequenced samples are indicated by color (all positive samples in gray – H1N1pdm09_notSequenced; sequenced samples in black - H1N1pdm09_Sequenced) as shown in the key.

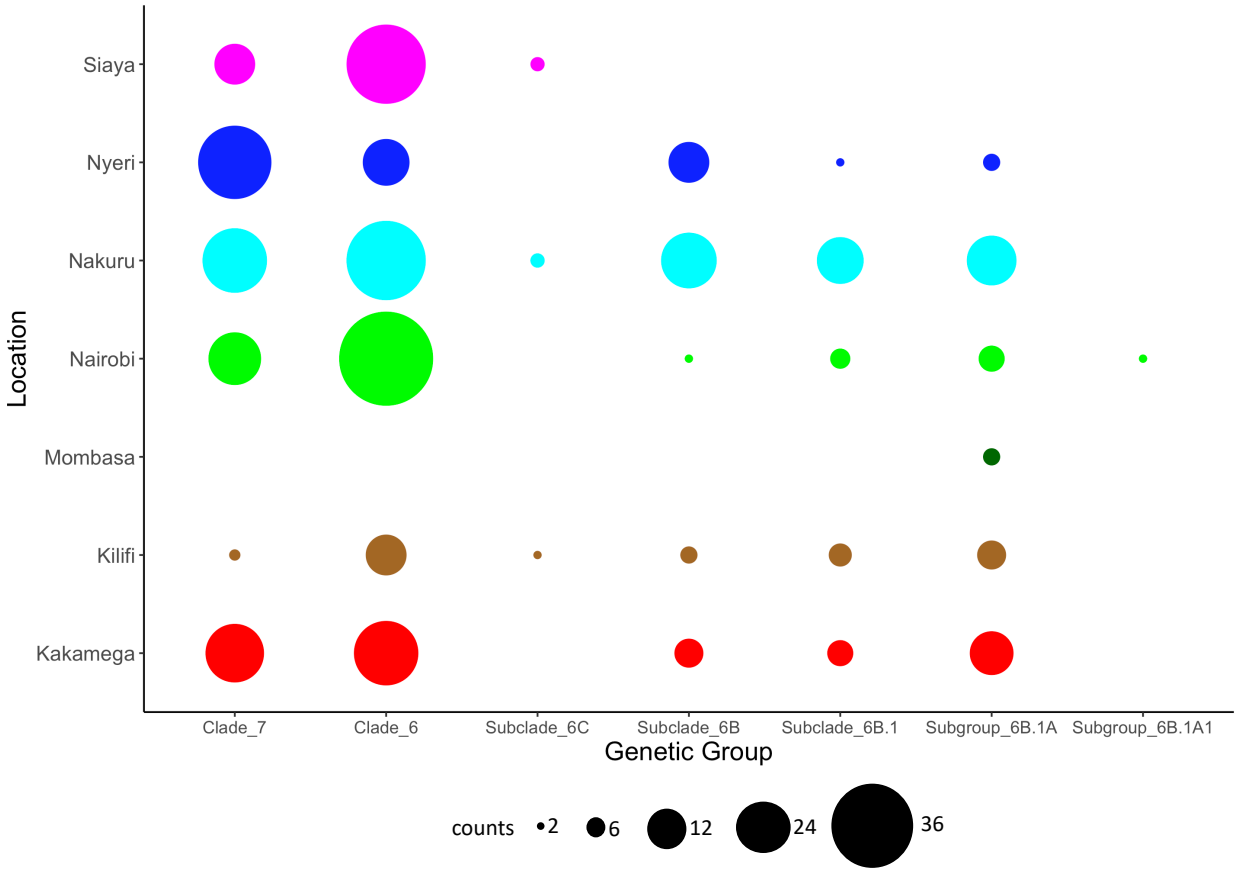


Figure 4.2: Bubble plot showing distribution of A(H1N1)pdm09 virus genetic groups by location in Kenya between 2009 and 2018. The size of the circle is proportional to the number of samples as shown in the counts key below the figure.

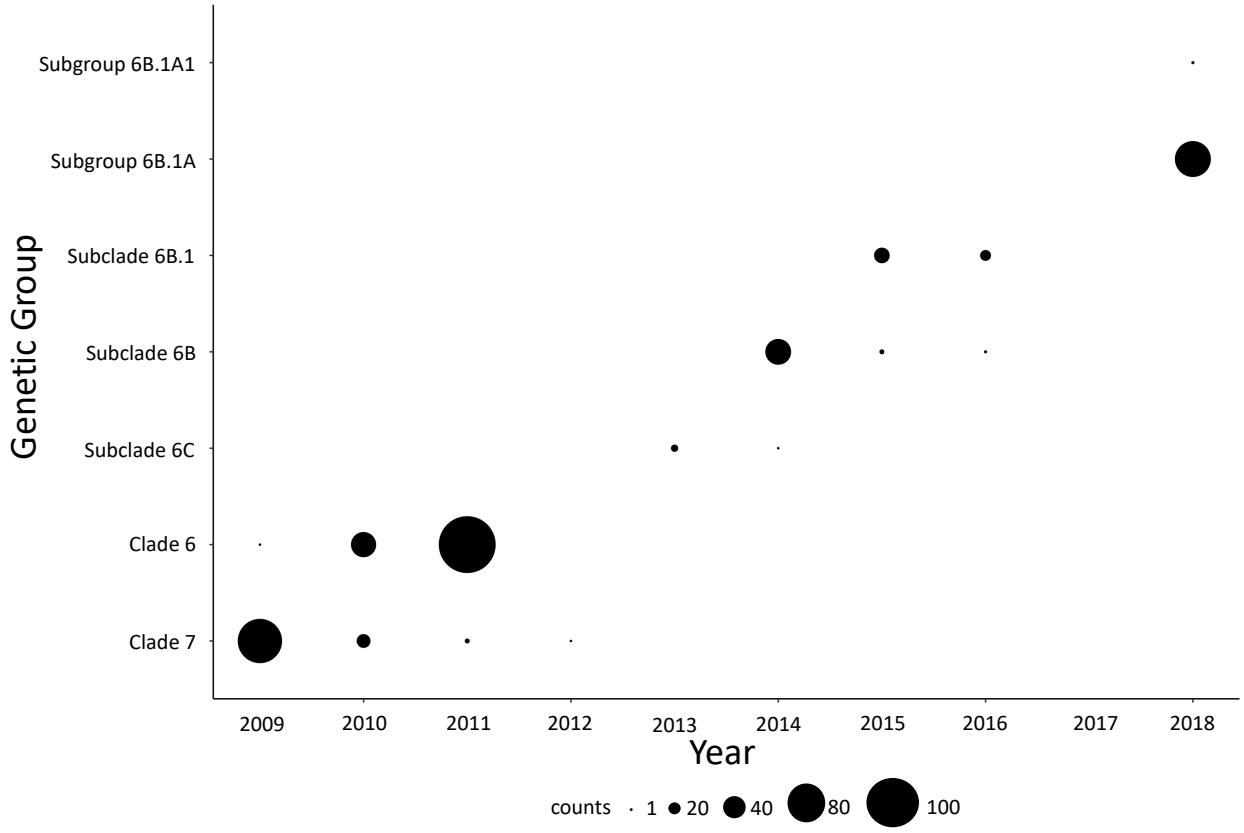


Figure 4.3: Bubble plot showing distribution of A(H1N1)pdm09 virus genetic groups by year of surveillance in Kenya between 2009 and 2018. The size of the circle is proportional to the number of samples as shown in the counts key below the figure.

4.3.3 Population Genetics of A(H1N1)pdm09 Virus

Analysis of the Kenyan and global A(H1N1)pdm09 virus WGS data phylogeny revealed a comb-like appearance during the early phase of the pandemic in 2009-10 (*Figure 4.4)*. This pattern suggests rapid increase in genetic diversity, which occurs in the absence of strong selective pressures whereby virus migration is determined by rapid spread and stochastic events. This behavior is expected of a virus population that infects a predominantly naïve local population upon its emergence. In contrast, post-pandemic A(H1N1)pdm09 viruses isolated since 2011 exhibited a ladder-like phylogeny, which is characteristic of viruses subject to continuous antigenic drift typical of human seasonal influenza viruses. This change in evolutionary pattern coincided with the emergence of 2 distinct A(H1N1)pdm09 virus lineages from 2011 onwards, although 1 of these lineages went extinct, resulting in the global circulation of a single dominant lineage in 2018.

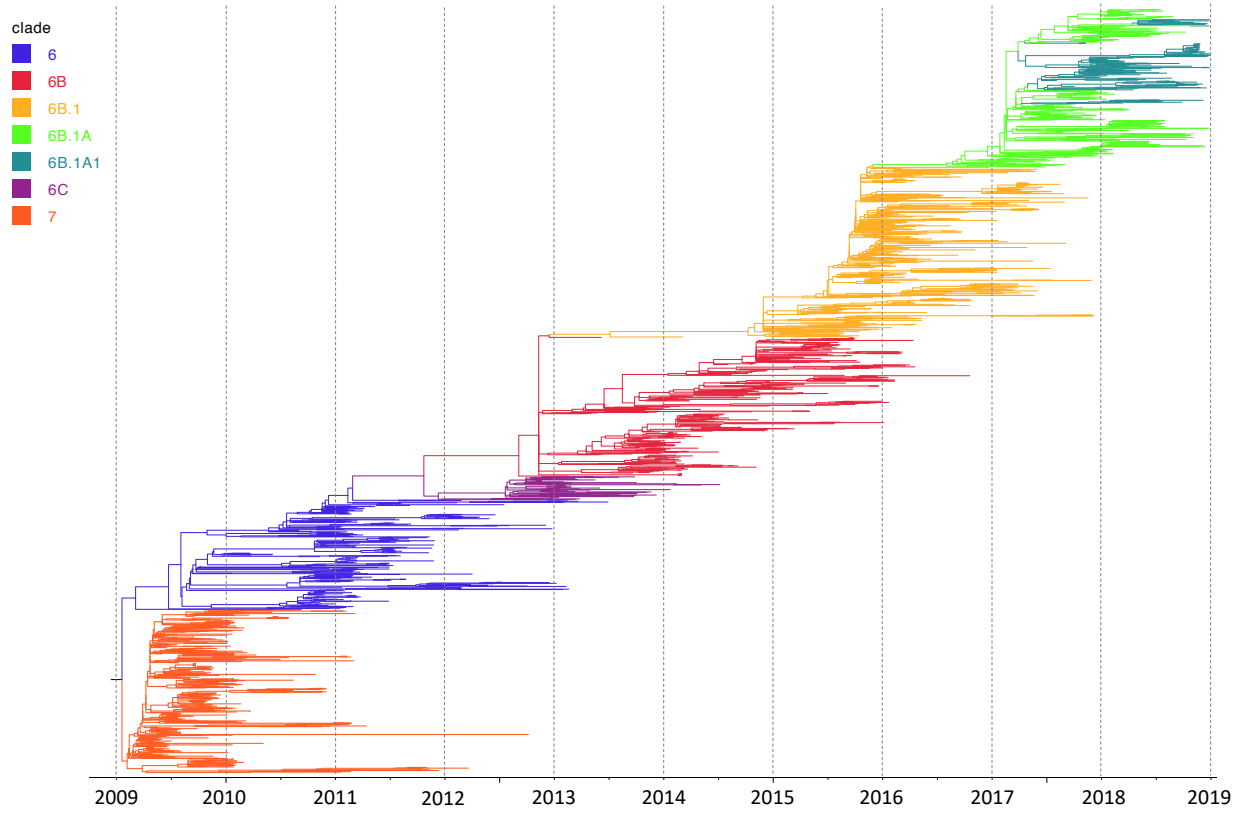


Figure 4.4: Time-resolved maximum-likelihood phylogenetic tree of 1,970 human influenza A(H1N1)pdm09 virus whole-genome sequences from Kenya and global locations collected between 2009 and 2018 with branches colored by genetic group.

4.3.4 Population Dynamics of A(H1N1)pdm09 Virus in Kenya, 2009-2018

Coalescent reconstruction of the pandemic in Kenya, using WGS data from Kenya only, revealed oscillating patterns in relative genetic diversity of A(H1N1)pdm09 virus after an initial rapid increase during the early phase of the pandemic, which broadly corresponded to winter patterns in the northern and southern hemispheres (*Figure 4.5)*. These patterns were associated with relatively lower levels of relative genetic diversity and biannual epidemic peaks that corresponded to the seasonal outbreaks in the northern and southern hemispheres. These results suggest that after its emergence in Kenya, the A(H1N1)pdm09 virus rapidly adapted to form seasonal epidemic patterns typical of seasonal influenza viruses. These patterns are associated with biannual epidemic peaks and initially corresponded to epidemic patterns in the temperate regions, which exhibited rapid increase in relative genetic diversity followed by distinct seasonal bottlenecks. Despite the earliest reports of A(H1N1)pdm09 virus from Kenya starting in late June 2009, the relative genetic diversity peaked in November 2009 (*Figure 4.5)*, which suggests that the initial outbreak was limited in spread and duration.

Variation in seasonal intensity was observed with smaller epidemics seen in mid-2010, mid-2011 and mid-2013, with virus diversity markedly reduced in 2012-13 and 2016-17. Very little A(H1N1)pdm09 virus activity was also observed in 2012, 2013, and 2016. Scrutiny of surveillance data of IAV and influenza B virus from 2009-18 indicates that the smaller epidemics of A(H1N1)pdm09 virus were correlated with higher incidences of A(H3N2) and influenza B viruses (Chapter One, *Figure 1.5)*. For example, A(H3N2) virus was dominant in mid-2010 whereas influenza B was dominant in mid-2011 and mid-2013 when the smaller epidemics of A(H1N1)pdm09 virus were observed in the country. This suggests that the seasonal patterns of A(H1N1)pdm09 virus took longer to be established in Kenya where very little A(H1N1)pdm09

virus activity was observed in some years, which corresponded to local epidemics being dominated by influenza A(H3N2) and influenza B viruses, respectively throughout the country.

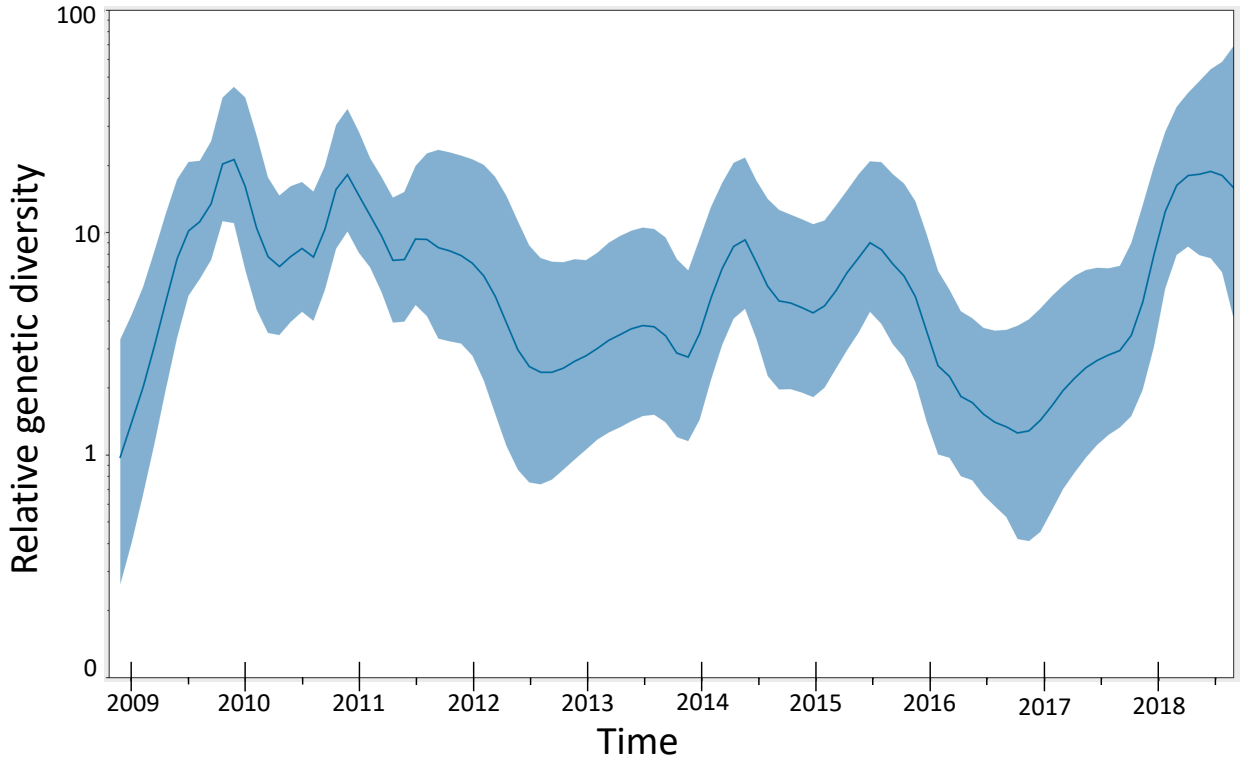


Figure 4.5: Relative genetic diversity of influenza A(H1N1)pdm09 virus from Kenya, 2009-18, resolved using the Gaussian Markov Random Field (GMRF) model. Solid lines in the GMRF plot represent the mean relative genetic diversity through time, while the corresponding shaded areas indicate the 95% highest posterior density intervals.

4.3.5 Estimation of Number of A(H1N1)pdm09 Virus Introductions into Kenya

Ancestral state reconstruction for geographical region of internal nodes in the phylogenies of clusters consisting of A(H1N1)pdm09 viruses from Kenya allowed identification of specific internal nodes that represented virus introductions into the country; this was based on 2 discrete states, which represent transitions from non-Kenyan to Kenyan states. The estimated dates of these introductions were inferred from corresponding internal nodes for the WGS data phylogeny, which provided evidence for introductions of A(H1N1)pdm09 viruses into Kenya during the pandemic period in 2009-10.

Kenya-specific transmission chains were identified using 3 established criteria: (i) the cluster must be significantly supported with a phylogenetic bootstrap of >80%; (ii) the cluster must contain more than 2 isolates; and (iii) more than 80% of isolates within the cluster must be sampled within Kenya, *Figure 4.6*. Clusters were named to reflect their placement within the global genetic clades 1-7, for example, KENA-GC7 indicates Kenyan cluster A viruses that fall within global genetic clade 7 viruses. By this criteria, 8 Kenyan clusters were identified during the 2009-10 pandemic period within genetic clades 6 and 7 (KENA-GC7, KENB-GC7, KENC-GC7, KEND-GC7, KENE-GC7, KENF-GC6, KENG-GC6 and KENH-GC6), each consisting of 3 to 95 isolates, which represented 8 independent introductions of A(H1N1)pdm09 viruses into Kenya. Therefore, the conclusion was that there were at least 8 independent introductions of A(H1N1)pdm09 viruses into Kenya during 2009-10.

The majority of pandemic virus transmission clusters in 2009-10 season persisted in Kenya, for example, KENA-GC7 that consisted of viruses sampled between July 2009 and December 2010. This provides evidence for the persistence of individual transmission clusters of A(H1N1)pdm09 viruses in a specific locality. Using geographical locations of the individuals from whom samples

were obtained (in the context of the genetically defined transmission clusters) the spatial patterns of migration of A(H1N1)pdm09 viruses within Kenya were examined during the pandemic. All the transmission clusters were represented by isolates from all 6 sampled locations (Nairobi, Nakuru, Nyeri, Siaya, Kakamega, and Kilifi) during the early phase of the pandemic, which suggests extensive virus spread among all the sampled locations in Kenya in 2009. Additionally, transmission clusters that persisted from 2009 to 2010 consisted of viruses sampled across the whole country, which suggests that A(H1N1)pdm09 virus persistence in Kenya was not constrained geographically.

In the post-pandemic period (2011 onwards), multiple introductions of A(H1N1)pdm09 virus genetic groups into Kenya were observed, as seen from state transitions in the ancestral state reconstruction, *Figure 4.6*. The following transmission clusters, which represent multiple independent introductions into Kenya for the different genetic groups of A(H1N1)pdm09 viruses, were observed: subclade 6C - KENI-GC6C and KENJ-GC6C; subclade 6B - KENK-GC6B, KENL-GC6B, KENM-GC6B, KENN-GC6B and KENO-GC6B; subclade 6B.1 - KENP-GC6B.1 and KENQ-GC6B.1; subgroup 6B.1A – KENR-GC6B.1A, KENS-GC6B.1A, KENT-GC6B.1A, and KENU-GC6B.1A; subgroup 6B.1A1 - KENV-GC6B.1A1.

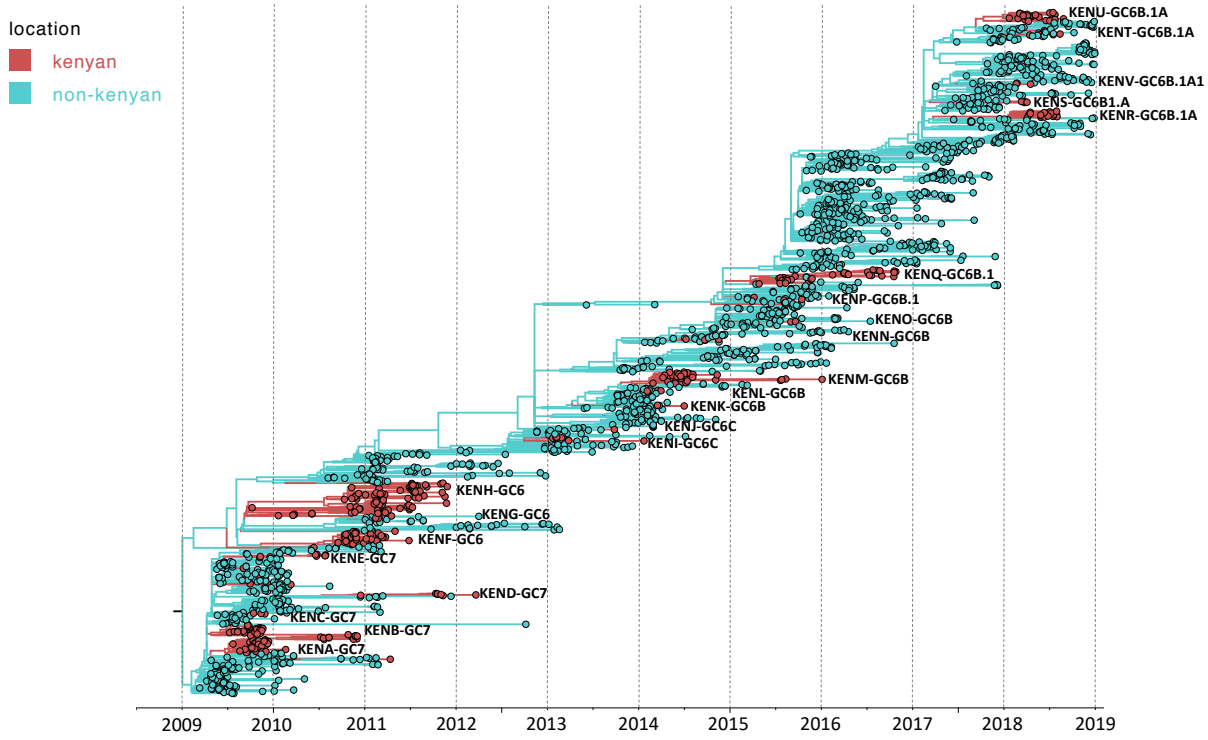


Figure 4.6: Time-resolved maximum-likelihood phylogenetic tree of Kenyan and contemporaneous global WGS data collected from 2009 to 2018. Unique Kenyan clusters are labeled with the prefix KEN, followed by A(H1N1)pdm09 virus cluster grouping and genetic group, for example, KENA-GC7 indicates Kenya cluster A viruses, which fall within global genetic clade 7 of A(H1N1)pdm09 virus. The Kenyan clusters are shown for all the genetic groups identified in Kenya from 2009 to 2018 and provides evidence for multiple introductions of A(H1N1)pdm09 viruses into Kenya throughout the study period. Kenyan viruses are colored in red whereas global viruses are colored in blue as per the key.

4.3.6 Local and Global Phylogenies of A(H1N1)pdm09 Virus

Having observed multiple introductions of A(H1N1)pdm09 viruses into Kenya over the study period, additional investigations sought to identify the global sources of these introductions into Kenya through reconstruction of global phylogenies. Phylogenetic analysis of 383 virus WGS from this study and 1,587 contemporaneous global WGS data revealed extensive geographical mixing of A(H1N1)pdm09 viruses at both hemispheric and continental scales of observation (*Figure 4.7* and *4.8)*. There was extensive global mixing of A(H1N1)pdm09 viruses, with co-circulation of viruses from Kenya with those from all northern and southern hemisphere regions including in countries in Africa, Asia, Europe, North America, South America, and Oceania.

Closer examination of the phylogenies of sequences from Africa showed evidence for the presence of strongly supported sub-lineages consisting predominantly of strains from Kenya but also containing strains from Tanzania and Ethiopia, (*Figure 4.9*, panel (A)); this is indicative of viral traffic between these border sharing countries. Strains from Africa fell into some strongly supported multinational lineages with strains from eastern Africa (Tanzania), central Africa (Congo and Rwanda), and southern Africa (Zambia), which suggests possible migration of A(H1N1)pdm09 viruses throughout the African continent, (*Figure 4.9*, panel (B)). Additionally, viruses from Africa fell into some regional lineages consisting of viruses from western Africa (Mali, Burkina Faso, and Ivory Coast); (*Figure 4.9*, panel (C)), southern Africa (South Africa and Mozambique); (*Figure 4.9*, panel (D)), and central Africa (Congo and Rwanda); (*Figure 4.9*, panel (E)).

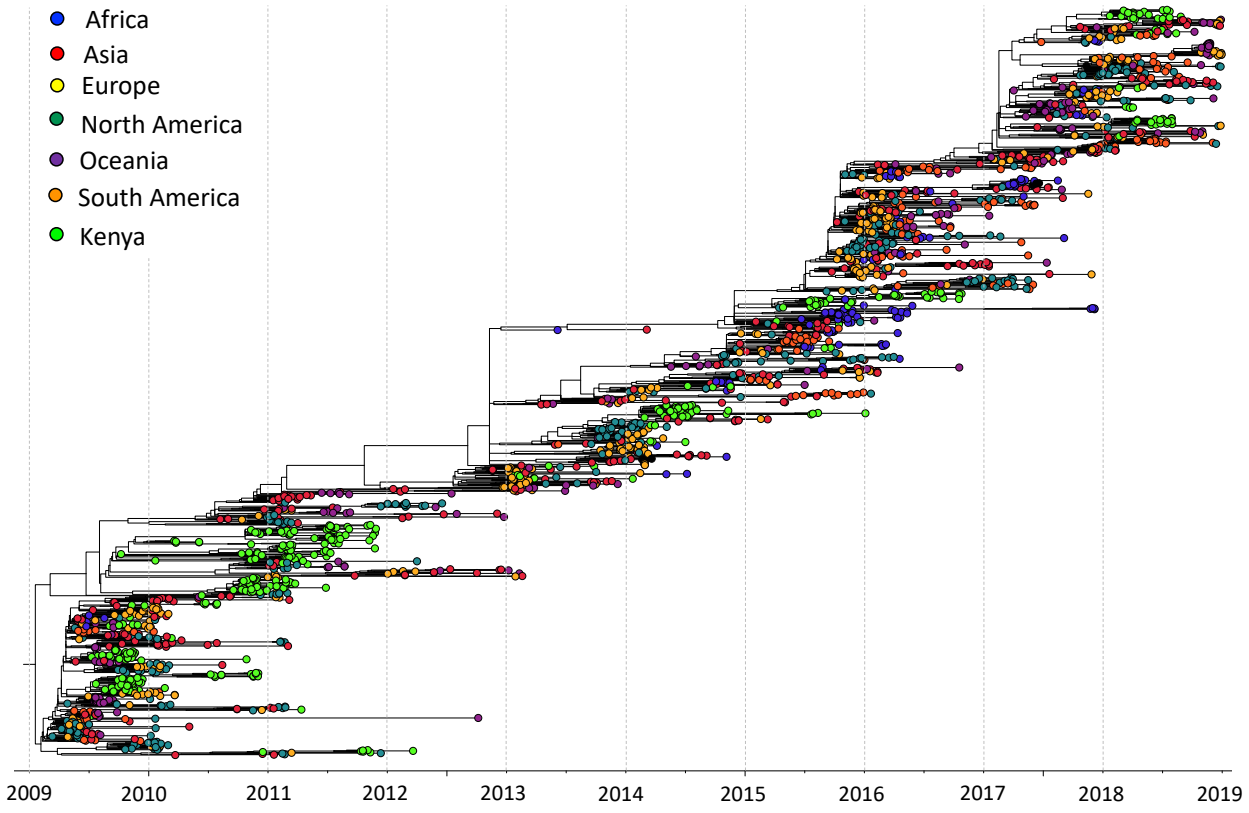


Figure 4.7: Time-resolved maximum-likelihood phylogeny of whole-genome sequences of influenza A(H1N1)pdm09 viruses from Kenya and other global locations showing sequences from Kenya, Africa, Asia, Europe, North America, South America, and Oceania.

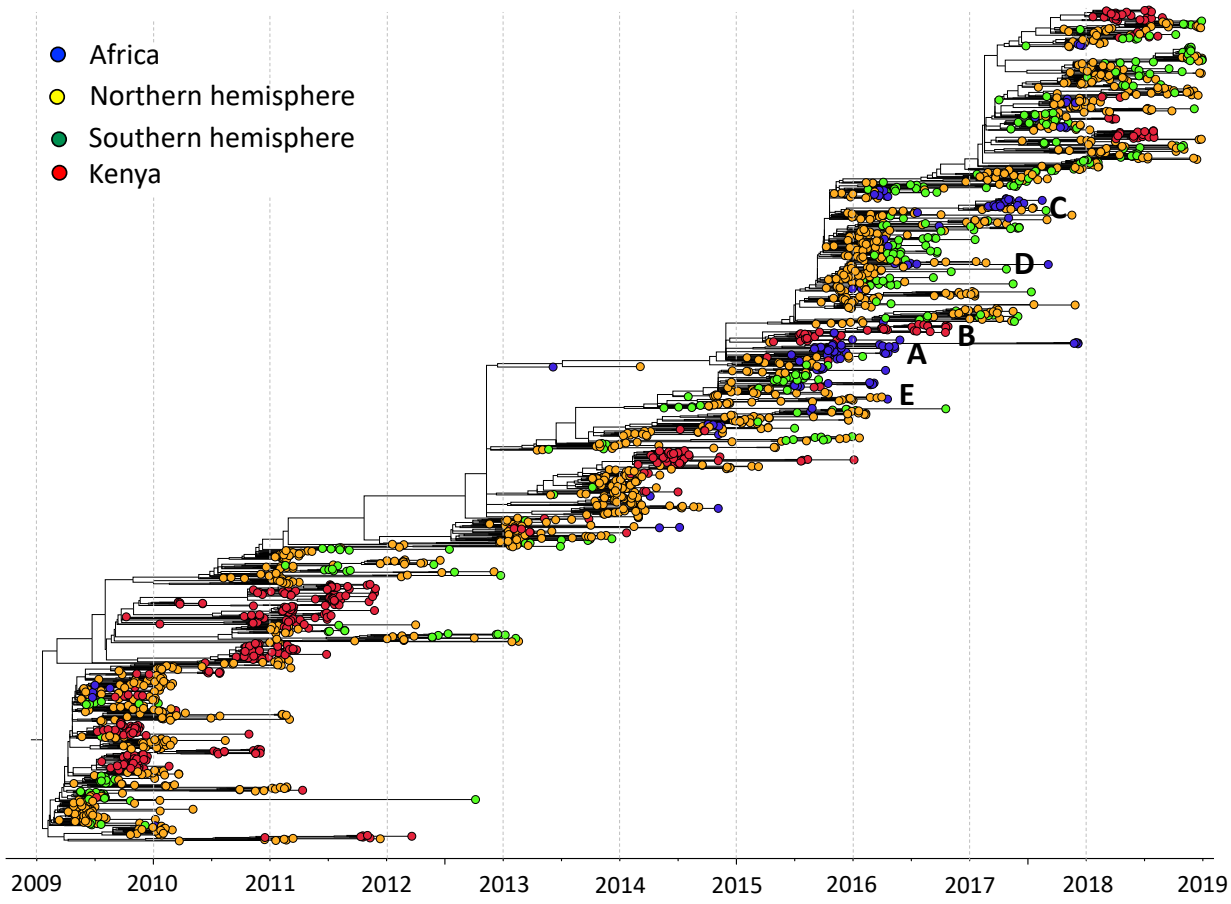


Figure 4.8: Time-resolved maximum-likelihood phylogeny of whole-genome sequences of influenza A(H1N1)pdm09 viruses from Kenya and other global locations showing Kenyan, African, and northern and southern hemisphere region genomes. The clusters consisting of A(H1N1)pdm09 virus genetic group sub-lineages, multinational lineages and regional lineages as labelled in Figure 4.9 are labeled (A, B, C, D, and E).

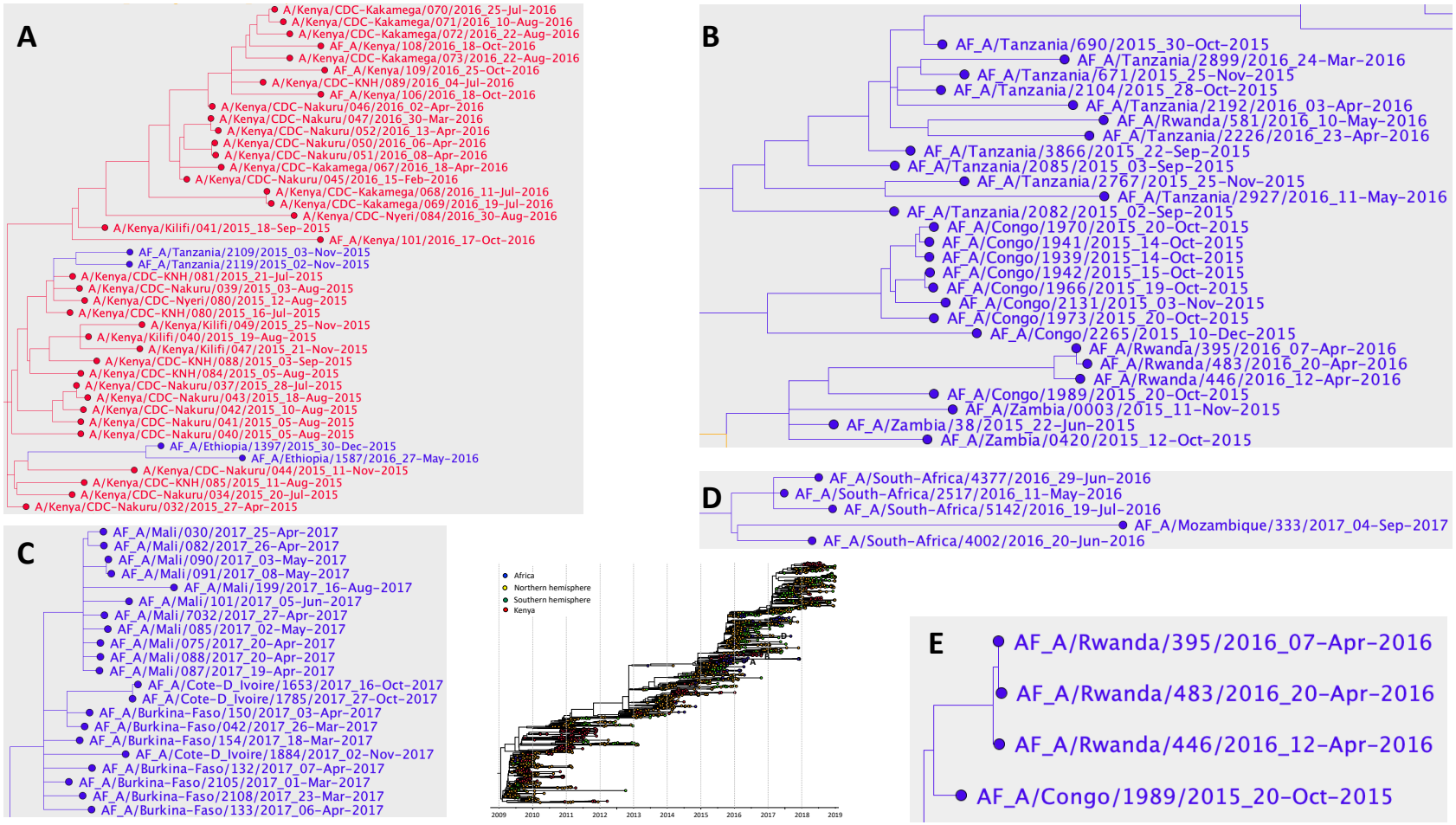


Figure 4.9: Time-resolved maximum-likelihood phylogeny of influenza A(H1N1)pdm09 viruses from Kenya and global locations showing exploded views of clusters consisting of viruses from Kenya and Africa. The figure shows: (A) cluster of viruses from Kenya, Ethiopia, and Tanzania; (B) cluster of viruses from Tanzania, Congo, Rwanda, and Zambia; and (C) cluster of viruses from western Africa (Mali, Burkina Faso, and Cote D'Ivoire), (D) southern Africa (South Africa and Mozambique), and (E) central Africa (Congo and Rwanda), respectively.

4.3.7 Local Spread of A(H1N1)pdm09 Virus in Kenya, 2009-2018

The phylogeography of A(H1N1)pdm09 virus in Kenya was reconstructed using BSSVS models to capture the underlying spatial migration dynamics of the virus among a set of 7 geographical locations in Kenya (Kakamega, Kilifi, Mombasa, Nairobi, Nakuru, Nyeri, and Siaya); *Figure 4.10*. Significant migration rates from Nyeri (0.81-0.93) into most locations including Nairobi, Nakuru, Kilifi, and Mombasa were observed, *Table 4.1*. Virus migration from Nakuru to Nyeri was also significant. Additionally, very strongly supported migration rates from Nakuru to Kilifi, and from Nairobi and Kilifi to Kakamega, respectively were observed. Strongly supported migration rates from Nakuru to Nairobi, and from Kilifi and Mombasa to Nyeri, respectively were also observed. Locations in proximity (for example, Nairobi, Nyeri, and Nakuru) also had well supported migration pathways for A(H1N1)pdm09 virus, *Figure 4.10*. The location states obtained by discrete phylogeographic reconstruction also revealed a strongly spatially structured Kenyan A(H1N1)pdm09 virus population (*Figure 4.11*), which can be observed from the clustering of viruses by sampling location across the country.

Table 4.1: Asymmetrical migration rates between location states in Kenya inferred using the BSSVS model for influenza A(H3N2) virus.

	Migration rates*						
†	Nairobi	Nakuru	Nyeri	Kakamega	Kilifi	Siaya	Mombasa
Nairobi	—	2.48	0.88	**1.11**	0.86	0.82	0.95
Nakuru	**1.7**	—	**2.24**	1.47	**1.21**	0.91	0.85
Nyeri	**0.91**	**0.91**	—	0.91	**0.81**	0.65	**0.93**
Kakamega	0.92	1.18	0.98	—	0.97	0.77	0.52
Kilifi	0.97	0.96	**0.98**	**0.98**	—	0.94	0.32
Siaya	0.91	0.62	0.98	0.87	0.97	—	**0.98**
Mombasa	0.93	0.95	**0.96**	0.96	0.95	0.93	—

*Migration rates in bold indicate supported rates with Bayes factor ≥3.

†Number of sequences: Nairobi, 66; Nakuru, 100; Nyeri, 59; Kakamega, 71; Kilifi, 39; Siaya, 43; and Mombasa, 5.

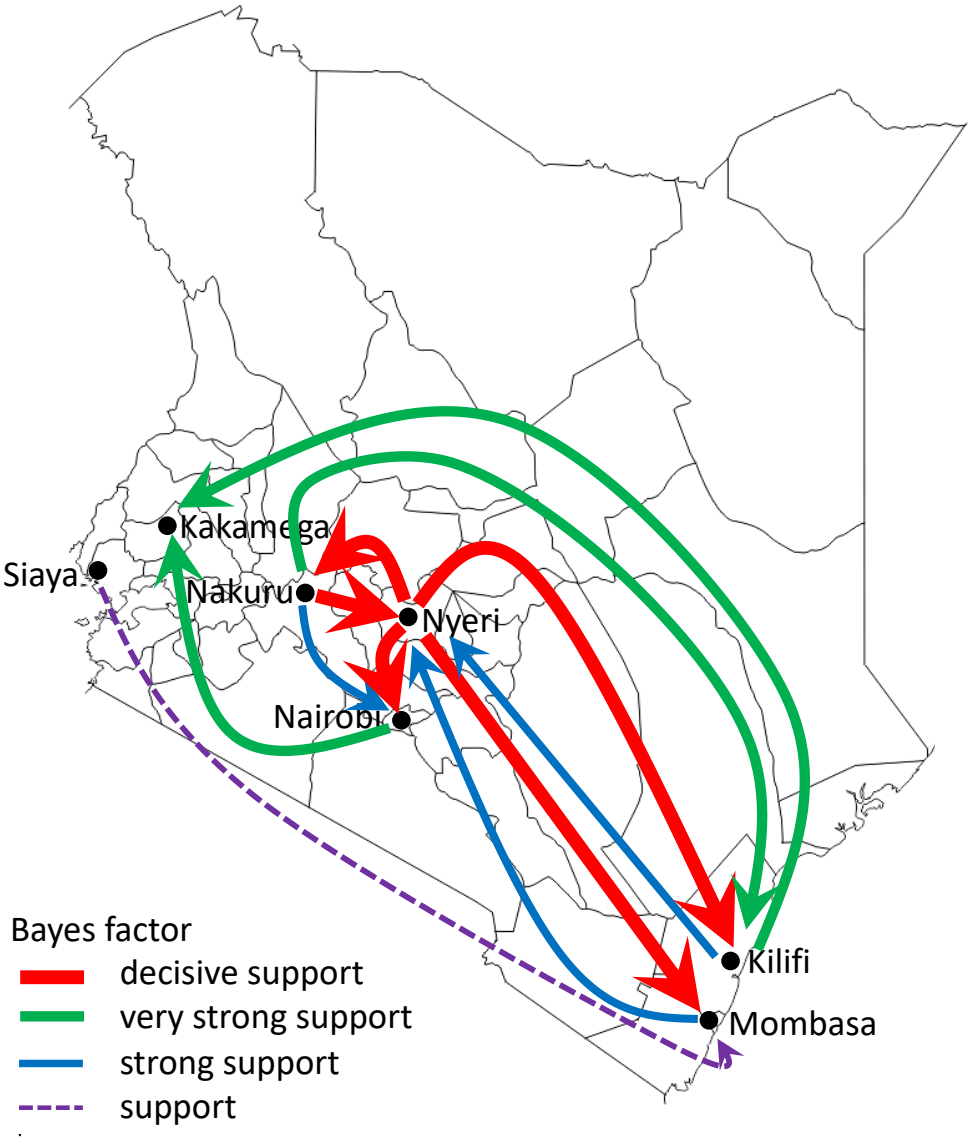


Figure 4.10: Migration networks of influenza A(H1N1)pdm09 virus reconstructed using sequence data from Kenya, 2009-2018. Asymmetric migration pathways between location states were inferred for Kenya locations. Coloured line arrows indicate significant migration routes from one location state to another, while line thickness represents the degree of statistical support. Red arrowed lines are shown to indicate decisive migration routes with Bayes factor (BF) support ≥1000; green lines represent very strongly supported routes with 100≤BF<1000; blue lines indicate strongly supported routes 10≤BF<100; and purple dotted lines indicate supported routes with 3≤BF<10.

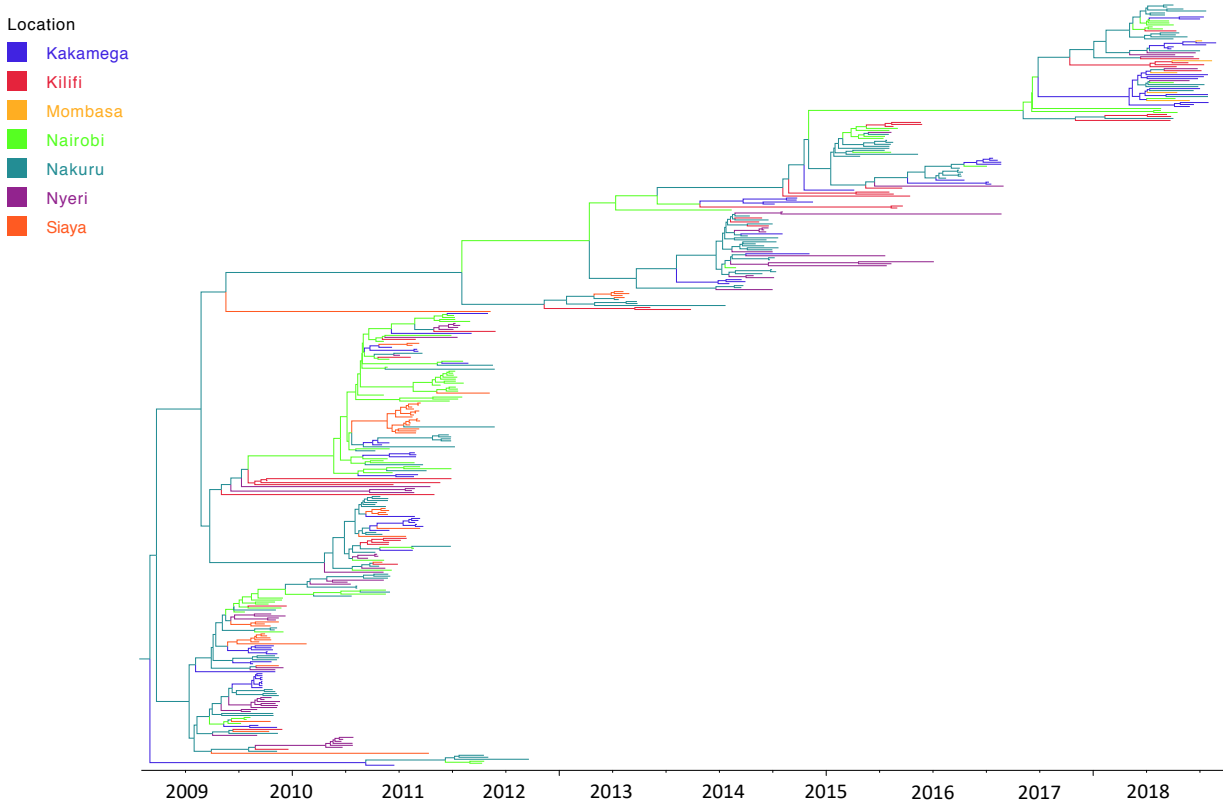


Figure 4.11: Time-resolved MCC trees inferred for WGS data of A(H1N1)pdm09 viruses from Kenya, 2009-18. MCC, maximum clade credibility; WGS, whole-genome sequencing.

4.4 Discussion

In this chapter, the phylogeographical analysis of A(H1N1)pdm09 virus is reported, which provides a detailed overview of the introduction and spread of the virus in Kenya since its global emergence in March-April 2009. The results were obtained from genomic analysis of samples collected globally from March 2009 to December 2018, including 383 WGS data collected in Kenya from June 2009 to December 2018. The analysis provides a finer resolution of the patterns of introductions of A(H1N1)pdm09 viruses into Kenya particularly during the 2009 pandemic period and the global source population of virus introductions into the country. This novel work on understanding the introduction and spread of A(H1N1)pdm09 viruses in Kenya was conducted by reconstructing the phylogeographic history of the virus in a discrete space (Lemey et al., 2009a) and ancestral state reconstruction for geographical region of internal nodes to define the geographic ancestry of the viruses (Sagulenko et al., 2018).

Reconstruction of the past population dynamics revealed oscillating patterns in relative genetic diversity of A(H1N1)pdm09 viruses in Kenya after an initial rapid increase during the early pandemic spread, which broadly corresponded to the winter patterns in the northern and southern hemispheres. These patterns were associated with relatively lower levels of relative genetic diversity and biannual epidemic peaks that corresponded to the seasonal outbreaks in the two hemispheres. Similar patterns of lower levels of relative genetic diversity and biannual epidemic peaks were observed in other tropical countries, for example, in India, Brazil and Singapore (Su et al., 2015) during the pandemic. On the other hand, higher levels of relative genetic diversity were reported for temperate regions, with the observed biannual epidemic peaks in Kenya and other tropical regions corresponding to seasonal outbreaks in temperate regions during the pandemic (Su et al., 2015). These observations suggest that after its global emergence, A(H1N1)pdm09 viruses

rapidly adapted to form seasonal epidemic patterns typical of seasonal influenza viruses in all the countries including Kenya.

The temperate northern and southern hemisphere countries experienced two pandemic waves. In the temperate countries of the northern hemisphere, the pandemic strain emerged in the cooler months during which seasonal epidemics influenza viruses typically occur, which resulted in a first pandemic wave of moderate magnitude followed by a larger second in-season wave, for example, in the UK (Baillie et al., 2012; Galiano et al., 2011; Lycett et al., 2012), USA (CDC; Nelson et al., 2011), Europe (Amato-Gauci et al., 2011; Zehender et al., 2012), and Australia (Van Kerkhove and Mounts, 2011). In these countries, clear differences were observed between the two waves. For example, the first wave of infections in the UK was genetically complex and comprised of multiple co-circulating and genetically distinct lineages, which had been introduced independently into the UK from elsewhere while the second wave consisted of transmission chains that had persisted from the first wave (Baillie et al., 2012). Elsewhere, in the USA, clear spatial patterns were observed in the first wave of the pandemic in which strong founder effects resulted in genetically distinct viral clades sweeping through 3 main states in Spring of 2009. The spatial structure was subsequently disintegrated by extensive global mixing of A(H1N1)pdm09 viruses during the second wave in the Fall of 2009, which was dominated by a single clade that had been dominant in New York city in the first wave (Nelson et al., 2011). In contrast, both waves in temperate southern hemisphere countries occurred in-season with little difference in viral genetic structure (Fielding et al., 2015; Van Kerkhove and Mounts, 2011). Kenya and other tropical countries experienced a single epidemic wave, which may explain the lower levels of relative genetic diversity relative to the temperate countries, while the biannual epidemic peaks observed

in the tropics corresponded to the two pandemic waves observed in the temperate regions in both hemispheres.

The relative genetic diversity of A(H1N1)pdm09 virus in Kenya peaked in December 2009 despite the earliest reports of the virus from Kenya starting in late June 2009 (CDC, 2009a), which suggests that the initial outbreak was limited in spread and duration. Similar observations were made in the USA where the relative genetic diversity peaked in early December 2009 despite the earliest reports of the virus starting April 2009, which suggests limited spread and duration of the initial outbreak in the USA (CDC, 2009b; Su et al., 2015). Mexico exhibited the earliest peak in relative genetic diversity of A(H1N1)pdm09 virus (Su et al., 2015), consistent with the emergence of the epidemic in the Americas (CDC, 2009). Different geographical regions generated local epidemic peaks that matched with their respective annual winter seasons followed by seasonal genetic bottlenecks. For example, Europe and the USA showed increase in genetic diversity over winter months (Su et al., 2015) that is typical of seasonal influenza viruses whereas Kenya and other tropical countries exhibited biannual epidemic peaks corresponding to seasonal outbreaks in the temperate regions. Interestingly, the seasonal patterns took longer to be established in Kenya, which showed little or no A(H1N1)pdm09 virus activity is some years; these corresponded to local epidemics being dominated by A(H3N2) and influenza B viruses. Similar delays in the establishment of seasonal patterns of A(H1N1)pdm09 viruses were observed in other regions in which limited activity of A(H1N1)pdm09 viruses was experienced in some years, for example, in Japan (Su et al., 2015). Kenya experienced some variation in seasonal intensity of A(H1N1)pdm09 viruses with smaller epidemics observed in mid-2010, mid-2011 and mid-2013 while virus diversity was markedly reduced in 2012-13 and 2016-17. The country also experienced limited activity of A(H1N1)pdm09 viruses in 2012, 2013, and 2016, which corresponded with higher

incidences of influenza A(H3N2) and influenza B viruses. Similar observations were described for multiple global regions that were similarly dominated by smaller epidemics in mid-2010 and mid-2013; these smaller epidemics were associated with higher incidences and relative genetic diversity of influenza A(H3N2) and influenza B viruses (Su et al., 2015; Vijaykrishna et al., 2015).

Phylogenetic analysis revealed extensive global migration of A(H1N1)pdm09 viruses following the emergence with rapid and widespread mixing of Kenyan viruses with those from multiple global regions, which was associated with multiple introductions of A(H1N1)pdm09 viruses into Kenya during the pandemic and post-pandemic periods; these then established local transmission chains within Kenya. These continual introductions from the global population are emphasized by the relatively small number of clusters exclusively comprised of Kenyan strains in the global phylogeny of Kenyan and global virus sequences. The findings from this study are consistent with those of studies from other countries, which show regular introduction of new virus lineages and seeding of local seasonal epidemics (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015) and support the model of continuous migration of influenza viruses into and out of Kenya rather than a closed system in which viruses evolve entirely within the country. Mixing of viruses between all locations in Kenya and other countries also suggests virus migration into and out of Kenya outside the main air-transport hub of Nairobi, for example, through locations that border other countries in East Africa. Notably, there was evidence of virus migration between Kenya and its neighboring countries, although this conclusion was limited by the paucity of sequences from these neighboring countries. At the countrywide level, the spread of A(H1N1)pdm09 viruses is predominantly characterized by virus migration from multiple locations to multiple destinations within Kenya. Locations in proximity to each other were also characterized by strong migration pathways for the virus. Therefore, virus persistence in Kenya might be modulated by frequent

introductions of A(H1N1)pdm09 viruses from outside the country and virus migration between locations in proximity. Strains from Kenya fell into some strongly supported multinational lineages with strains from eastern, central and southern Africa, which suggests possible migration of A(H1N1)pdm09 viruses throughout the continent. Additionally, viruses from Africa fell into some regional lineages consisting of viruses from western Africa, central Africa and southern Africa, which suggests regional patterns of migration of A(H1N1)pdm09 viruses within the continent. However, there were fewer virus full genomes from sub-Saharan Africa during the study period to examine intra-African transmission dynamics in detail.

All Kenyan source viral lineages that seed peripheral locations in the country over the study period may not have sampled. Therefore, the suggestion of possible virus migration in and out of Kenyan locations outside the main air-transport hub of Nairobi, which is based on countrywide mixing of viruses between all locations must be interpreted carefully. Additionally, the paucity of virus sequence data from sub-Saharan African countries limited the analysis of virus migration dynamics and persistence patterns in the continent, which might have been useful to demonstrate an intra-continental migration dynamic. However, these findings have important implications for public health practice in Kenya and the region. For example, they suggest that future novel strains of influenza viruses may enter Kenya at multiple locations rather than just through its major airport-transport hub. Moreover, the rapid spread of influenza viruses throughout Kenya, even in remote rural regions of coastal and western Kenya, provides evidence for rapid dissemination of IAV once introduced into a country. The rapid and widespread migration of global influenza viruses into Kenya and the widespread global mixing with viruses from other countries as shown in this study emphasize that vaccine recommendations in either hemispheres need well distributed, widespread global sampling of influenza viruses from as many localities as possible.

CHAPTER FIVE

5 Phylogeography of Influenza A(H1N1)pdm09 and A(H3N2) Viruses in Africa, 2011-2013

5.1 Introduction

The acute nature of influenza virus epidemics suggests that the long-term circulation of influenza viruses in humans is driven by the global migration of the viruses (Petrova and Russell, 2018). Various hypotheses have been proposed to explain the global migration dynamics of influenza viruses, which have mainly been based on phylogenetic analysis of virus sequence data. First, the "source-sink" model for circulation of influenza viruses postulates that countries have putative tropical sources of influenza viruses that are characterized by year-round (or multi-annual) transmission, local persistence of influenza virus lineages, and relatively high virus genetic diversity. It is then proposed that influenza virus lineages migrate and seed seasonal epidemics in cooler temperate regions, where they experience inter-seasonal extinction (Rambaut et al., 2008). Therefore, epidemics in temperate climates are not typically sustained but are re-established by importation of viral lineages from tropical populations with more persistent transmission (Nelson et al., 2007; Rambaut et al., 2008). Second, seeding of viruses from E-SE Asia, whose hypothesis is attributed in part due to the perceived historical importance of E-SE Asia as a source of several pandemics and seasonal epidemics (Bedford et al., 2010; Bedford et al., 2015; Russell et al., 2008) and the sheer magnitude of the human population in E-SE Asia (United Nations, 2019). For example, annual A(H3N2) virus epidemics globally result from the introduction of new genetic variants from E-SE Asia, where viruses circulate through a network of temporally overlapping epidemics (Bedford et al., 2010; Bedford et al., 2015; Kosakovsky Pond et al., 2010; Lemey et al.,

2014; Russell et al., 2008) rather than local persistence (Nelson et al., 2007; Rambaut et al., 2008; Russell et al., 2008).

An alternative hypothesis proposes the existence of temporally migrating metapopulations of influenza viruses in which new virus strains can emerge in any geographical region with the location of the source population changing regularly (Bahl et al., 2011). In the model, virus migration into E-SE Asia occurs throughout the year with the migration contributing to the local persistence in those regions; multiple regions may therefore act as a potential source population for influenza virus epidemics (Bahl et al., 2011). Most recently, the global migration patterns of seasonal influenza viruses were shown to vary with the rate of antigenic evolution of different influenza virus types and subtypes (Bedford et al., 2015). For example, unlike A(H3N2) viruses that migrate globally from E-SE Asia and India each year, A(H1N1) and influenza B viruses sporadically persist locally between epidemics in multiple global regions, which gives rise to multiple co-circulating genetic lineages that occasionally result in divergent antigenic variants. In addition, the differences in the global dynamics of seasonal influenza viruses are likely a result of differences in rates of virus evolution (Bedford et al., 2015).

However, the role of tropical/sub-tropical low-to-middle income countries in the global migration dynamics of influenza viruses remains unclear due to insufficient data (Ng and Gordon, 2015; Viboud et al., 2013) especially in sub-Saharan Africa despite the high disease burden (Gessner et al., 2011; Katz et al., 2012b). The studies which proposed the different models for global migration of influenza viruses acknowledged the lack of virus sequence data from Africa, South and Central Asia, and South America in their inference of migration patterns as a major study limitation (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Rambaut et al., 2008; Russell et al., 2008). Therefore, the complete understanding of the global migration of influenza viruses requires deeper

and wider sampling from understudied tropical and sub-tropical regions, for example, Africa (Viboud et al., 2013). For example, additional analysis of influenza surveillance data from India led to the discovery that the global source region for A(H3N2) viruses also includes India in addition to E-SE Asia (Bedford et al., 2015) and confirmed previous hypotheses (Russell et al., 2008). Identification of a geographical source of new antigenic and genetic variants of influenza viruses could potentially improve early detection and prediction of new vaccine strains (Viboud et al., 2013).

WGS data for A(H1N1)pdm09 and A(H3N2) viruses were used to investigate the role of tropical and sub-tropical Africa in the global migration of IAV. WGS data for A(H1N1)pdm09 and A(H3N2) viruses from the PERCH-Africa study, newly generated WGS data for A(H1N1)pdm09 virus from Kenya, and contemporaneous global WGS data were used to investigate the global migration of A(H1N1)pdm09 and A(H3N2) viruses in a Bayesian statistical framework. A key aspect of the PERCH-Africa study is that it involved continuous, active, year-round, multi-country surveillance over several seasons that enabled the capture of any inter-seasonal strains.

5.2 Methods

5.2.1 African IAV Sample Details and Sequencing

A total of 127 IAV positive samples collected from August 2011 to January 2014 from 5 sites in 5 African countries (Basse, The Gambia; Bamako, Mali; Kilifi, Kenya; Soweto, South Africa; and Lusaka, Zambia) were received for the current study (see Chapter Two section 2.3.5). Initial sample screening for influenza A(H1N1)pdm09 and A(H3N2) viruses, nucleic acid extraction, IAV genome amplification, and genome assembly were performed as described in Chapter Two (sections 2.5.1, 2.5.2, 2.5.3, and 2.6.4).

5.2.2 Global Genome Sequence Dataset Collation

Global A(H1N1)pdm09 virus and A(H3N2) virus WGS datasets used in this study were all retrieved from the GISAID database and processed as described in Chapter Two, section 2.7.2. Briefly, all WGS data sampled from March 2009 to December 2018 for A(H1N1)pdm09 virus and from January 2009 to December 2016 for A(H3N2) virus were downloaded from GISAID. Duplicate sequences, sequences with missing dates (collection date and month), incomplete sequences, and sequences with ambiguous nucleotides (N) were all removed (Chapter Two, section 2.7.2). Representative sequences were binned by year and continent. For geographic regions with large datasets, intermittent sequences were randomly selected using in-house scripts while for underrepresented geographic regions, all available WGS data were included to overcome ascertainment bias. The dataset was then subset into 2010 to 2013 and 2014 to 2016 datasets; the 2010 to 2013 dataset was used for this analysis. For A(H1N1)pdm09 virus, the final dataset of 458 global sequences sampled from January 2010 to December 2013 was available (numbers in parenthesis indicate number of sequences): Africa (13); Asia (149); Europe (84); North America (170); South America (3); Oceania (39). An additional 125 A(H1N1)pdm09 virus WGS data generated from the SPReD-Kenya study between 2010 and 2013 were included in the A(H1N1)pdm09 virus analysis. For A(H3N2) virus, the final dataset of 761 global sequences sampled from January 2010 to December 2013 was available (numbers in parenthesis indicate number of sequences): Africa (7); Asia (198); Europe (41); North America (178); South America (199); Oceania (138).

5.2.3 Phylogenetic Analysis

Consensus nucleotide sequences were aligned and translated in AliView v1.26 (Larsson, 2014) and the individual genome segments were concatenated into full-length genomes using

SequenceMatrix (Vaidya et al., 2011). Phylogenetic trees of A(H1N1)pdm09 virus and A(H3N2) virus WGS data from PERCH-Africa, Kenya and contemporaneous global sequences were constructed with maximum-likelihood and bootstrap analysis of 1,000 replicates. The best-fit nucleotide substitution models were inferred using IQ-TREE v1.6.11 (Kalyaanamoorthy et al., 2017; Nguyen et al., 2014) and those chosen by the BIC for each concatenated virus genome implemented. The phylogenetic trees of A(H1N1)pdm09 virus and A(H3N2) virus WGS data were visualized and annotated using Figtree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

5.2.4 Spatial Dynamics of IAV Spread and Ancestral State Reconstruction

Phylogeographical analysis was conducted to assess the spread of A(H1N1)pdm09 and A(H3N2) viruses in the African continent and the global spread of the viruses using methods implemented in BEAST v1.10.4 package (Suchard et al., 2018). The analysis was implemented with an asymmetric discrete trait approach and applied the BSSVS model (Lemey et al., 2009a). To reduce the complexity of the MCC, location states were categorized as follows: (i) for IAV spread in the African continent, countries were used as location states for the country-wide analyses while two location states, “northern hemisphere” or “southern hemisphere”, were used for the hemisphere states analysis; (ii) for the global spread, 3 discrete location attributes were used: “region” - Africa, Asia, E-SE Asia, Europe, North America, South America, or Oceania; “hemisphere” - northern hemisphere or southern hemisphere; and “global location” - African or non-African. Phylogeographic inferences were visualized with the SPREAD3 software v0.9.7.1c package (Bielejec et al., 2016). To visualize the geographic spread of the virus over time, a D3 file was generated using SPREAD3 v0.9.7.1c package. The different MCMC chains were run until convergence, which ranged from 200 to 500 million generations, with sampling every 50,000 generations. Convergence was assessed, and the runs were combined after removing appropriate

burn-in using LogCombiner v1.10.4. The MCC trees with annotations were then visualized using Figtree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). Africa and global geo.json files were used for visualization of the African and global spread, respectively. The resulting log files were used to calculate the estimated IAV migration rates between locations and BF values for significant migration rates between discrete locations: ≥1,000 was deemed as decisive support, 100≤BF<1000 as very strong support, 10≤BF<100 as strong support, and 3≤BF<10 as supported.

Seven discrete geographical location states ("Africa", "Asia", "E-SE Asia", "Europe", "North America", "South America", or "Oceania") were used for ancestral state reconstruction for the geographical region of internal nodes of phylogenies. This was estimated using African and contemporaneous global sequences from other continents to determine the geographic ancestry of A(H1N1)pdm09 and A(H3N2) viruses using time-resolved phylogenies in TreeTime (Sagulenko et al., 2018).

Analysis files and scripts can be found on GitHub: https://github.com/DCollinsOwuor/H1N1pdm09_and_H3N2_viruses_Africa_and_global_phylogeography.

5.3 Results

5.3.1 IAV Whole-Genome Sequencing and Assembly

A total of 4,232 NP/OP swab samples were collected and tested for a range of respiratory pathogens, including IAV, from cases aged 1-59 months admitted to hospital with WHO-defined severe and very severe pneumonia (pre-2013 definition) and age-group matched controls without pneumonia randomly selected from communities surrounding the study sites. A total of 127 (3.0%) IAV positive specimen, which had not been previously subtyped for IAV, were received from all

the PERCH-Africa study sites. Of the 127 IAV positive specimen received, 100 (78.7%) IAV specimens that passed pre-sequencing quality control checks were loaded onto the Illumina MiSeq with corresponding success in generating WGS data for 31 (31%) A(H1N1)pdm09 and 69 (69%) A(H3N2) viruses, respectively, following sequencing and genome assembly (*Appendix 7.2.3*).

Between 54,000 and 1,550,000 short reads were available per sample, of which IAV-specific reads ranged between 1,900 to 1,140,000 reads (each of 250 bases); *Appendix 7.2.3*. All the genome assemblies were 13,133 nucleotides in length with mean depth of base coverage per genome ranging from 36 to 21,700 (calculated from, for example, [1,114,000 reads X 250 bases]/13,133). With regards to sequence availability in GISAID, these are among the first geographically and temporally comprehensive representation of seasonal IAV generated from sub-Saharan Africa using high-throughput technologies. Therefore, my project made an important contribution to the available sequence data from the continent, which can be used to improve understanding of the phylogeography of IAV in Africa and worldwide.

5.3.2 Circulation Patterns of Influenza A(H1N1)pdm09 Virus in Africa

5.3.2.1 Global Phylogeny of Influenza A(H1N1)pdm09 Virus

The global sources of introductions of A(H1N1)pdm09 virus into Africa were identified through reconstruction of global phylogenies of the virus. Phylogenetic analysis of 169 African WGS data (31 WGS data from PERCH-Africa study, 125 WGS data from the SPReD-Kenya study, and 13 WGS data from Africa) and 445 contemporaneous global A(H1N1)pdm09 virus WGS data from other continents revealed extensive geographical mixing of A(H1N1)pdm09 viruses from Africa with those from all northern and southern hemisphere regions, with co-circulation of viruses from Africa with those from countries in Asia, Europe, North America, South America, and Oceania (*Figure 5.1)*.

Closer examination of the phylogenies of sequences from Africa revealed evidence for presence of strongly supported African sub-lineages, which consisted predominantly of strains from the same geographical regions, for example, in southern Africa (South Africa and Zambia) and in western Africa (The Gambia and Mali); *Figure 5.2*, panels (A) and (B), respectively. This is indicative of virus migration between countries within the same geographical regions of Africa. Additionally, strains from different countries and different regions of Africa fell into some strongly supported multinational lineages, for example, Kenya, South Africa, and Zambia, which suggests possible intra-continental spread of A(H1N1)pdm09 virus within Africa (*Figure 5.2*, panel (C)).

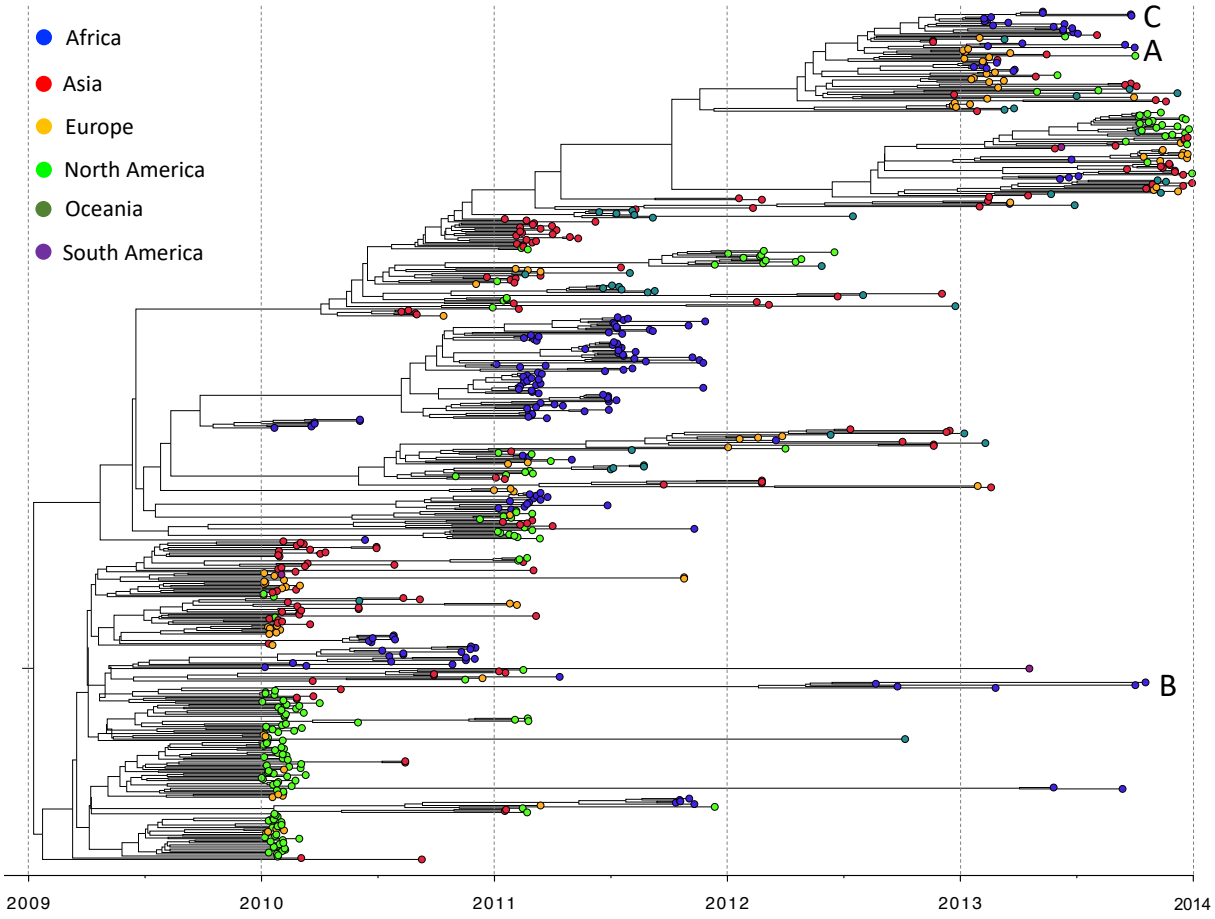


Figure 5.1: Time-resolved maximum-likelihood phylogeny of influenza A(H1N1)pdm09 viruses from Africa and other global continents showing sequences from Africa, Asia, Europe, North America, South America, and Oceania. The location of African sub-lineages and multinational lineages, as shown in Figure 5.2, are labelled (A, B, and C).

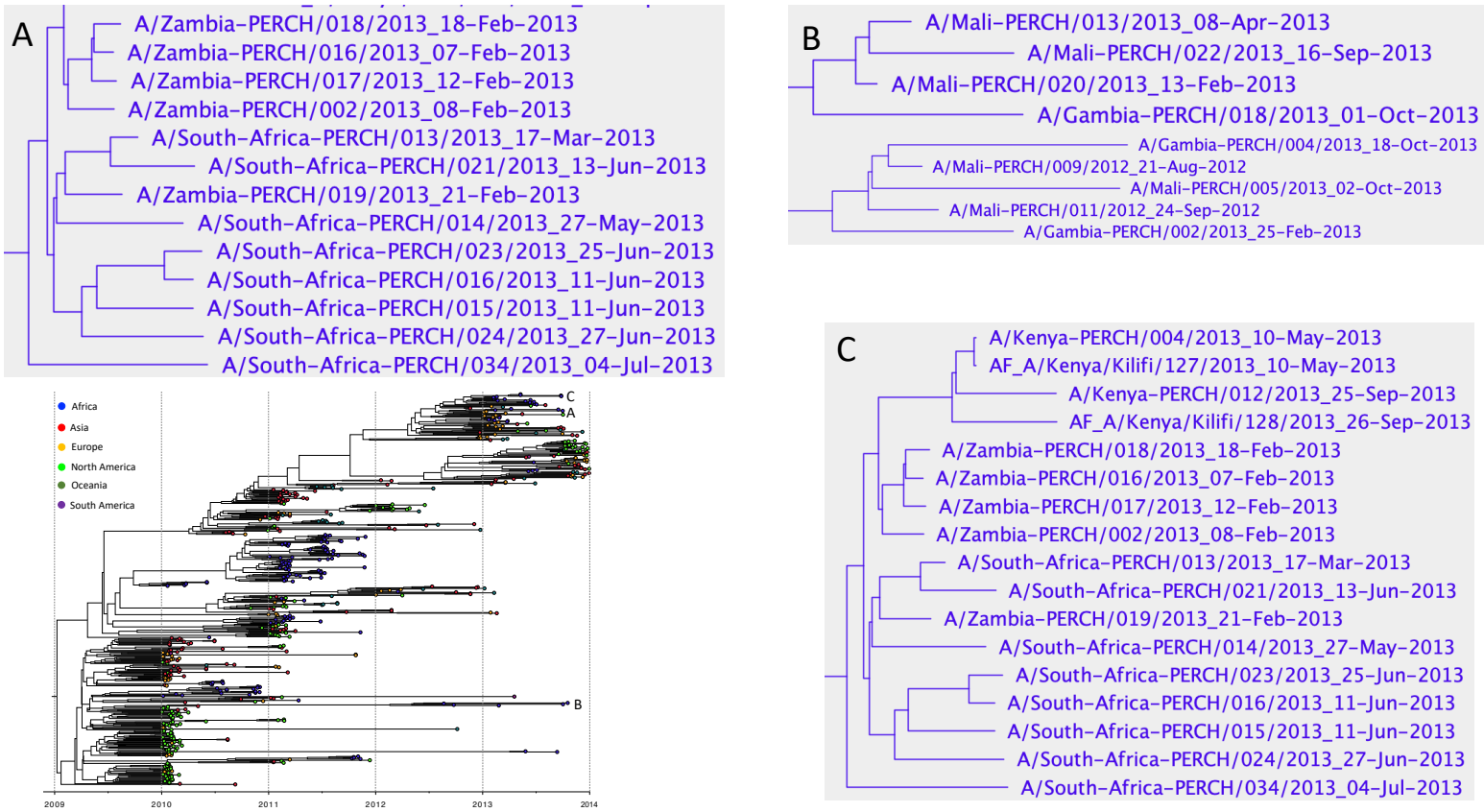


Figure 5.2: Time-resolved maximum-likelihood phylogeny of influenza A(H1N1)pdm09 viruses from Africa and other global locations showing exploded views of clusters consisting of viruses from Africa. The figure shows: (A) cluster of viruses from southern Africa (Zambia and South Africa; (B) cluster of viruses from western Africa (Mali and The Gambia); and (C) cluster of viruses from southern and eastern Africa (South Africa, Zambia, and Kenya).

5.3.2.2 Migration Patterns of Influenza A(H1N1)pdm09 Virus in Africa

The phylogeography of influenza A(H1N1)pdm09 virus in Africa was reconstructed using BSSVS models to capture the underlying spatial transmission dynamics of the virus across the continent at the countrywide and hemisphere scales of observation. Strongly supported migration pathways were observed for countries within the same geographical regions of the continent, for example, in western Africa (migration from Mali to The Gambia) (*Figure 5.3*, panel (A)). Significant migration pathways were also observed for different geographical regions in Africa, for example, from western Africa to southern Africa (migration from Mali to South Africa and Zambia) and from southern Africa to eastern Africa (migration from Zambia to Ethiopia and from South Africa to Kenya); *Figure 5.3*, panel (A). The best supported migration pathways were also determined for the northern and southern hemisphere regions, which revealed strong migration pathways from the northern to the southern hemispheres in the continent (*Figure 5.3*, panel (B)).

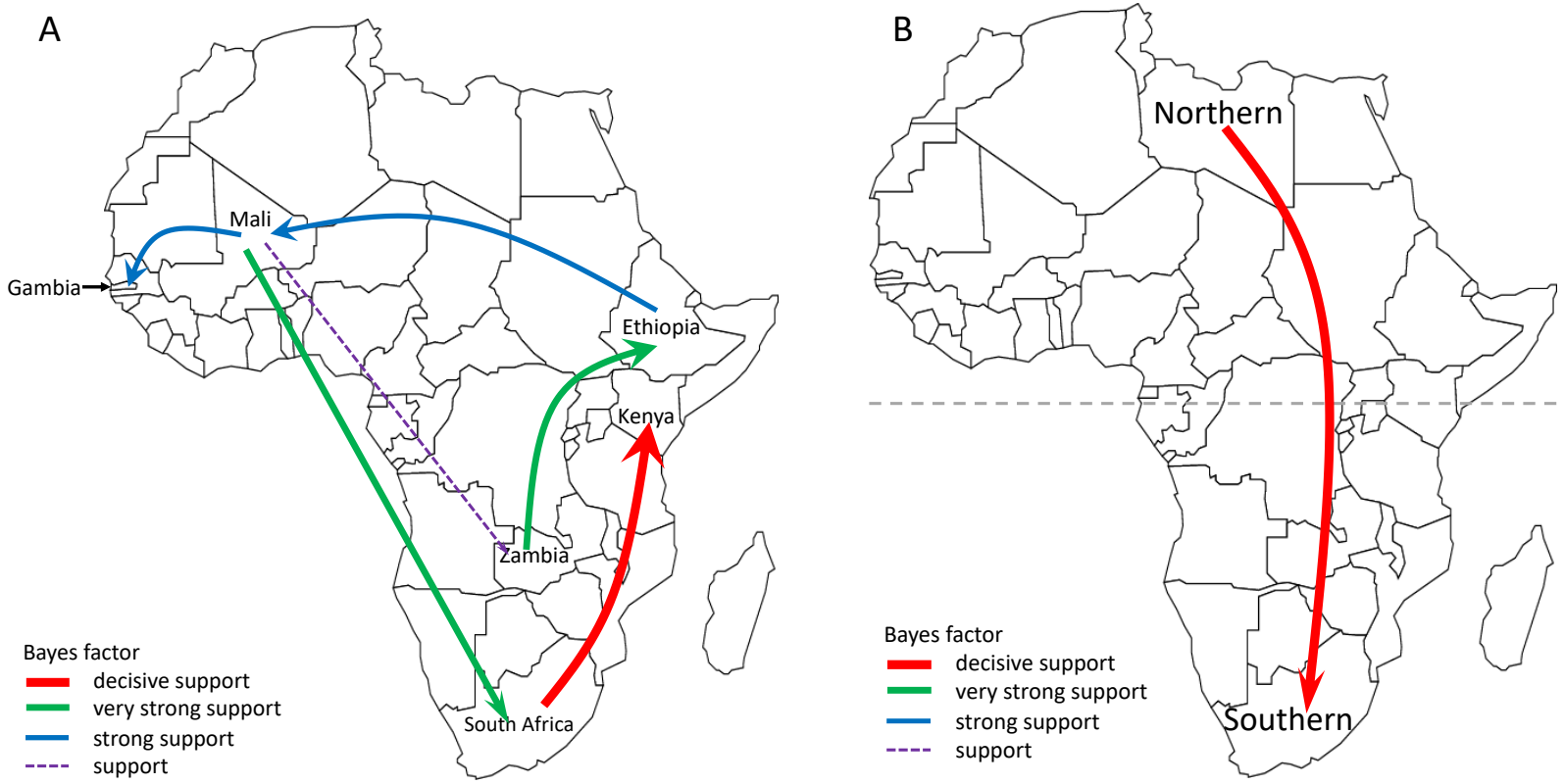


Figure 5.3: Migration networks of influenza A(H1N1)pdm09 virus in Africa reconstructed using sequence data from PERCH-Africa and SPReD-Kenya studies, and additional contemporaneous sequences from Africa, 2010 to 2013. Asymmetric migration pathways between location states were inferred for African countries and northern and southern hemisphere regions in panels (A) and (B), respectively. Coloured line arrows indicate significant migration routes from one location state to another, while line thickness represents the degree of statistical support. Red arrowed lines are shown to indicate decisive migration routes with Bayes factor (BF) support ≥1000; green lines represent very strongly supported routes with 100≤BF<1000; blue lines indicate strongly supported routes 10≤BF<100; and dotted lines indicate supported routes with 3≤BF<10.

5.3.3 Circulation Patterns of Influenza A(H3N2) Virus in Africa

5.3.3.1 Global Phylogeny of Influenza A(H3N2) Virus

The global sources of A(H3N2) virus introductions into Africa were identified through reconstruction of global phylogenies of the virus. Phylogenetic analysis of 76 African WGS data (69 WGS data from PERCH-Africa study and 7 WGS data from Africa) and 754 contemporaneous global A(H3N2) virus WGS data from other continents revealed extensive geographical mixing of A(H3N2) viruses from Africa with those from all northern and southern hemisphere regions, with co-circulation of viruses from Africa with those from countries in Asia, Europe, North America, South America, and Oceania (*Figure 5.4)*.

Closer examination of the phylogenies of sequences from Africa showed evidence for presence of strongly supported African sub-lineages, which consisted predominantly of strains from the same geographical regions, for example, in southern Africa (South Africa and Zambia) and in western Africa (The Gambia and Mali); *Figure 5.5,* panels (A) and (B), respectively. This indicates virus migration between countries within the same geographical regions. Additionally, strains from different countries fell into strongly supported multinational lineages, for example, Kenya, Uganda, South Africa, and Zambia, which suggests possible intra-continental spread of A(H3N2) virus within Africa (*Figure 5.5,* panel (C)) similar to observations reported for A(H1N1)pdm09 virus.

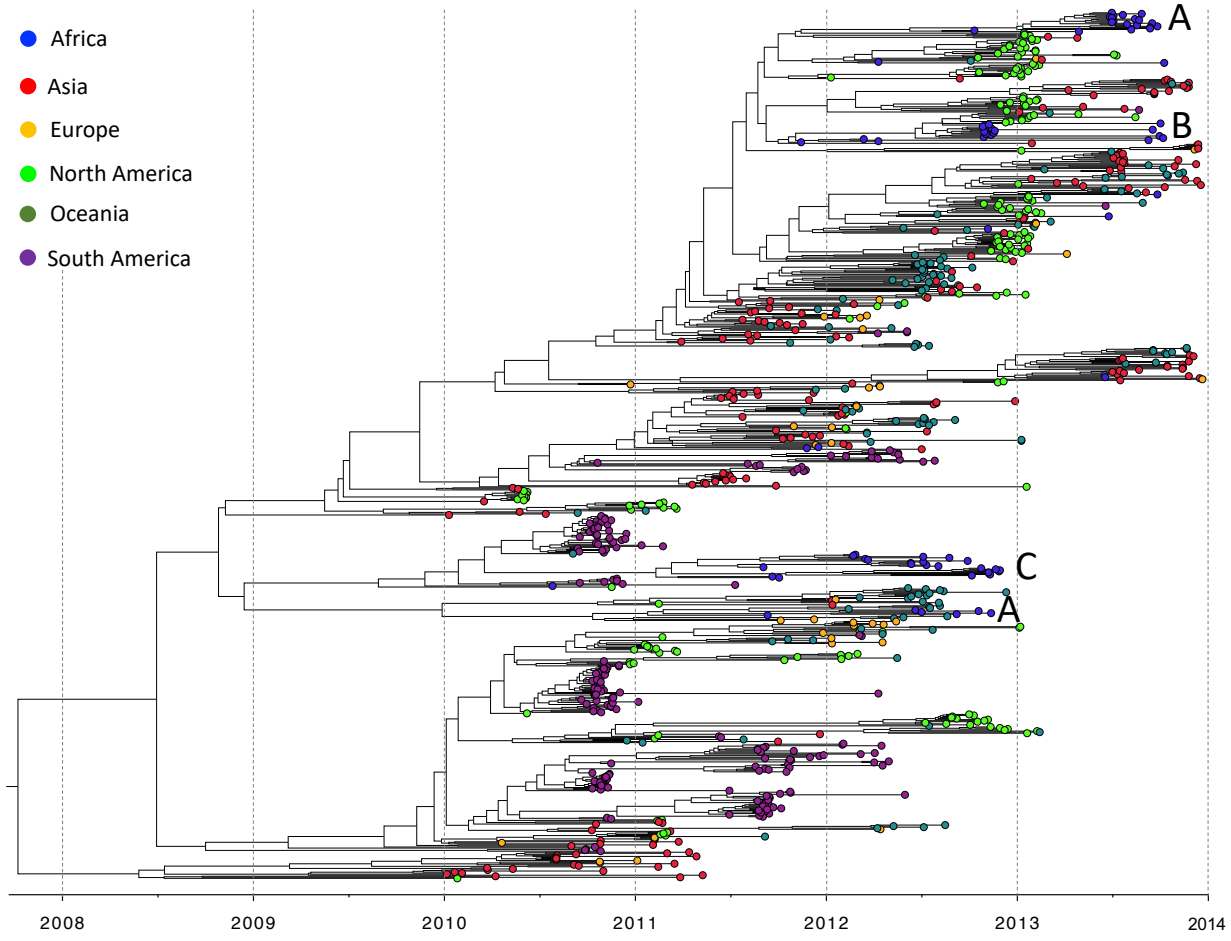


Figure 5.4: Time-resolved maximum-likelihood phylogeny of influenza A(H3N2) viruses from Africa and other global continents showing sequences from Africa, Asia, Europe, North America, South America, and Oceania. The location of African sub-lineages and multinational lineages, as shown in Figure 5.5, are labelled (A, B, and C).

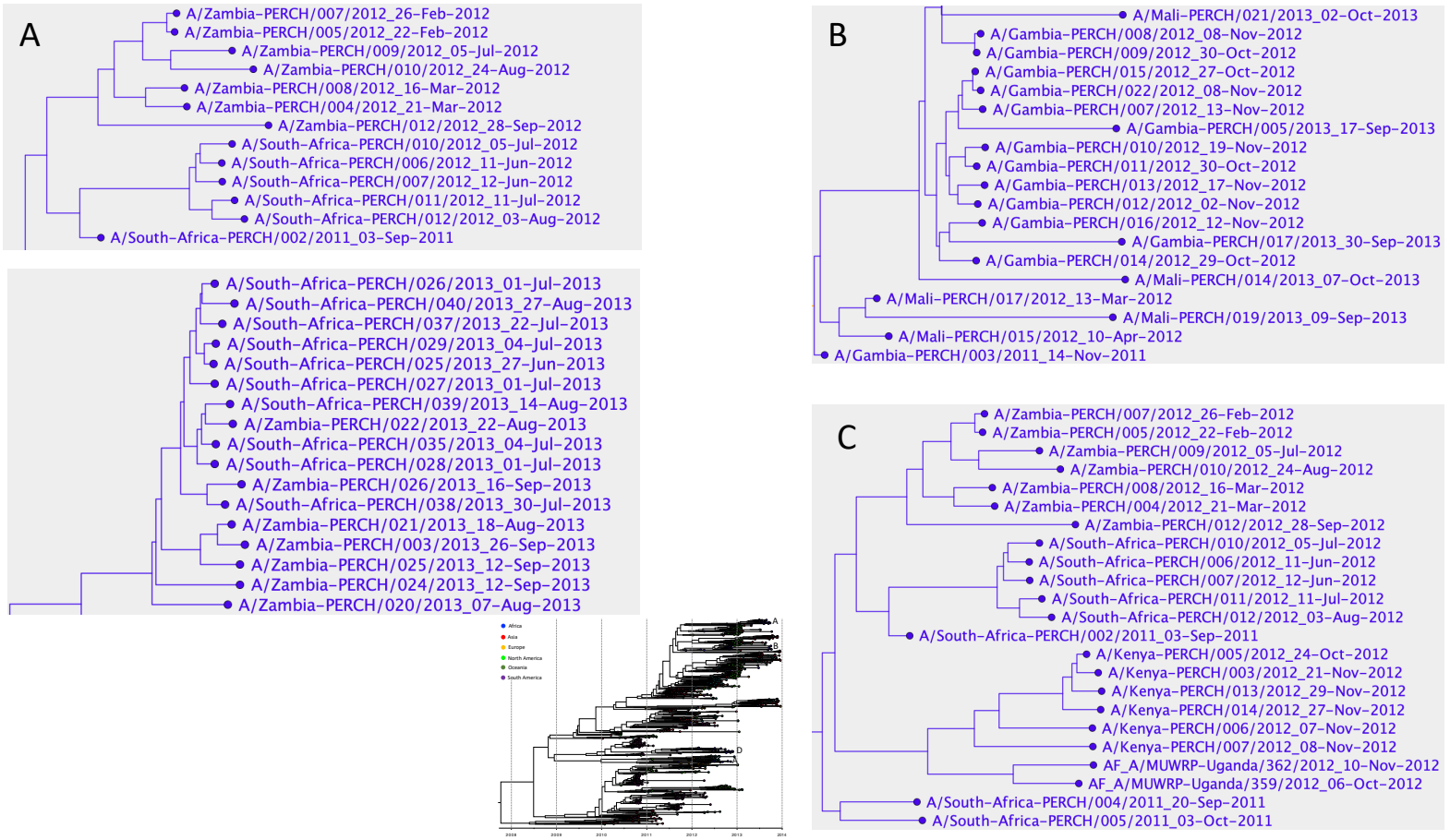


Figure 5.5: Time-resolved maximum-likelihood phylogeny of influenza A(H3N2) viruses from Africa and other global locations showing exploded views of clusters consisting of viruses from Africa. The figure shows: (A) cluster of viruses from southern Africa (Zambia and South Africa); (B) cluster of viruses from western Africa (Mali and The Gambia); and (C) cluster of viruses from southern and eastern Africa (South Africa, Zambia, Uganda, and Kenya).

5.3.3.2 Migration Patterns of Influenza A(H3N2) Virus in Africa

The phylogeography of influenza A(H3N2) virus in Africa was reconstructed using BSSVS models to reveal the underlying spatial transmission dynamics of the virus across Africa at the countrywide and hemisphere scales of observation. Strongly supported migration pathways were observed for countries within the same geographical regions of the continent, for example, in western Africa (migration between The Gambia and Mali), *Figure 5.6*, panel (A). Significant migration pathways were also observed for different geographical regions in Africa, for example, between southern and eastern Africa (migration from South Africa and Zambia to Kenya and from Kenya to South Africa and Zambia; *Figure 5.6*, panel (A). The best supported migration pathways were also estimated for the northern and southern hemisphere regions for A(H3N2) virus, which revealed strong migration pathways from the northern to the southern hemisphere (*Figure 5.6*, panel (B)) that is similar to the migration patterns observed for A(H1N1)pdm09 virus in Africa.

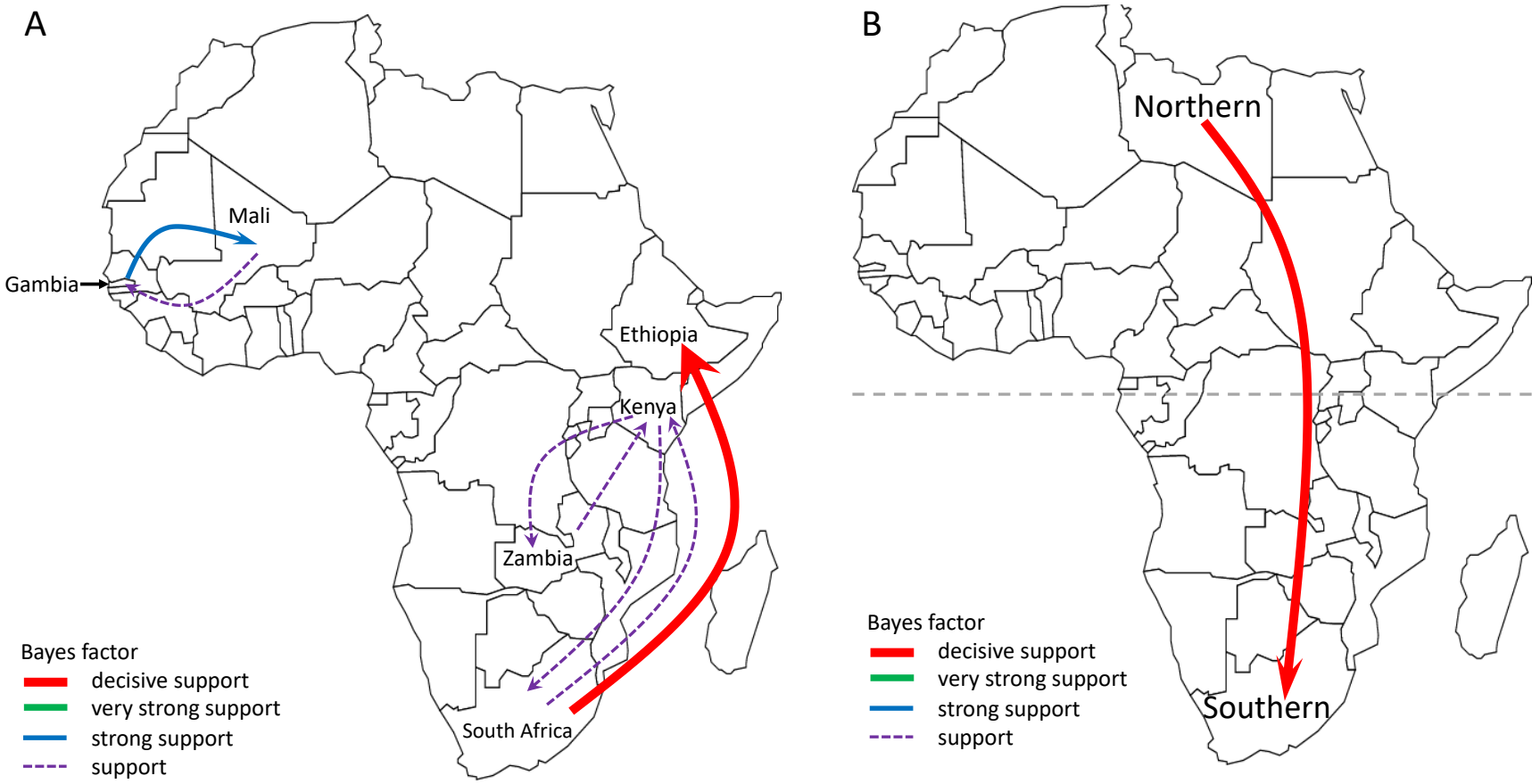


Figure 5.6: Migration networks of influenza A(H3N2) virus in Africa reconstructed using sequence data from PERCH-Africa and contemporaneous sequences from Africa, 2010 to 2013. Asymmetric migration pathways between location states were inferred for African countries and northern and southern hemisphere regions in panels (A) and (B), respectively. Coloured line arrows indicate significant migration routes from one location state to another, while line thickness represents the degree of statistical support. Red arrowed lines are shown to indicate decisive migration routes with Bayes factor (BF) support ≥1000; green lines represent very strongly supported routes with 100≤BF<1000; blue lines indicate strongly supported routes 10≤BF<100; and purple dotted lines indicate supported routes with 3≤BF<10.

5.3.4 Global Migration Dynamics of Influenza A(H1N1)pdm09 and A(H3N2) Viruses

The phylogeographical patterns of influenza A(H1N1)pdm09 and A(H3N2) viruses were reconstructed using BSSVS models to reveal the underlying global migration dynamics of the viruses. For A(H1N1)pdm09 virus, significant migration pathways from E-SE Asia (0.81-3) into multiple geographical regions including Africa, Asia, Europe, North America, and Oceania were observed. Additionally, significant migration pathways from North America (0.52-0.73) to E-SE Asia, Europe, and Oceania were observed, *Table 5.1*. The observed migration pathways corroborate these results, *Figure 5.7*. As such, these findings suggest that the global seeding of A(H1N1)pdm09 virus epidemics is driven by different geographical locations, which also includes Africa, where E-SE Asia and North America are major transmission sources. For A(H3N2) virus, significant migration pathways from E-SE Asia (0.62-0.34) into all other geographical regions including Africa, and from North America (0.6-1.63) to Europe, Oceania, and South America were observed, *Table 5.2*. The global migration pathways for A(H3N2) corroborate these results, *Figure 5.8*. As observed for A(H1N1)pdm09 virus, these findings suggest that the global seeding of A(H3N2) virus epidemics is driven by different geographical locations that also includes Africa in which E-SE Asia and North America are major transmission sources. A greater global migration (~7 decisive pathways) was observed for A(H3N2) virus compared to A(H1N1)pdm09 virus (~6 decisive pathways), consistent with greater global circulation of A(H3N2) virus compared to A(H1N1)pdm09 virus. Here, for the first time, the role of Africa in the global migration dynamics of influenza A(H1N1)pdm09 and A(H3N2) viruses is demonstrated using virus sequence data generated from my project, which has improved the understanding of the phylogeography of IAV in Africa and worldwide.

Table 5.1: Asymmetrical migration rates between global location states inferred using the BSSVS model for influenza A(H1N1)pdm09 virus.

	Migration rates*						
†	Africa	Asia	E-SE Asia	Europe	North America	Oceania	South America
Africa	—	0.97	0.95	0.97	0.98	0.96	0.99
Asia	0.96	—	**0.88**	0.83	0.99	0.95	0.95
E-SE Asia	**1.48**	**0.81**	—	**2.83**	**3**	**1.5**	0.89
Europe	0.93	0.94	0.95	—	0.95	0.95	**0.56**
North America	0.87	1.01	**0.52**	**0.73**	—	**0.58**	0.95
Oceania	0.84	0.88	0.86	0.81	0.87	—	0.88
South America	0.82	0.85	0.84	0.93	0.84	0.88	—

*Migration rates in bold indicate supported rates with Bayes factor ≥3.

†Number of sequences: Africa, 169; Asia, 17; E-SE Asia, 132; Europe, 84; North America, 170; South America, 3; and Oceania, 39.

Table 5.2: Asymmetrical migration rates between global location states inferred using the BSSVS model for influenza A(H3N2) virus.

	Migration rates*						
†	Africa	Asia	E-SE Asia	Europe	North America	Oceania	South America
Africa	—	0.98	0.97	0.99	0.69	0.79	0.97
Asia	0.91	—	0.92	0.92	0.96	0.96	0.93
E-SE Asia	**0.77**	**0.92**	—	**1.19**	**2.27**	**3.34**	**0.62**
Europe	0.93	0.97	0.97	—	0.9	0.96	0.93
North America	0.96	0.97	0.85	**0.6**	—	**1.63**	**0.93**
Oceania	0.87	0.94	**0.78**	**0.8**	0.98	—	0.98
South America	0.82	0.92	0.79	0.89	0.72	0.91	—

*Migration rates in bold indicate supported rates with Bayes factor ≥3.

†Number of sequences: Africa, 7; Asia, 17; E-SE Asia, 181; Europe, 41; North America, 178; South America, 199; and Oceania, 138.

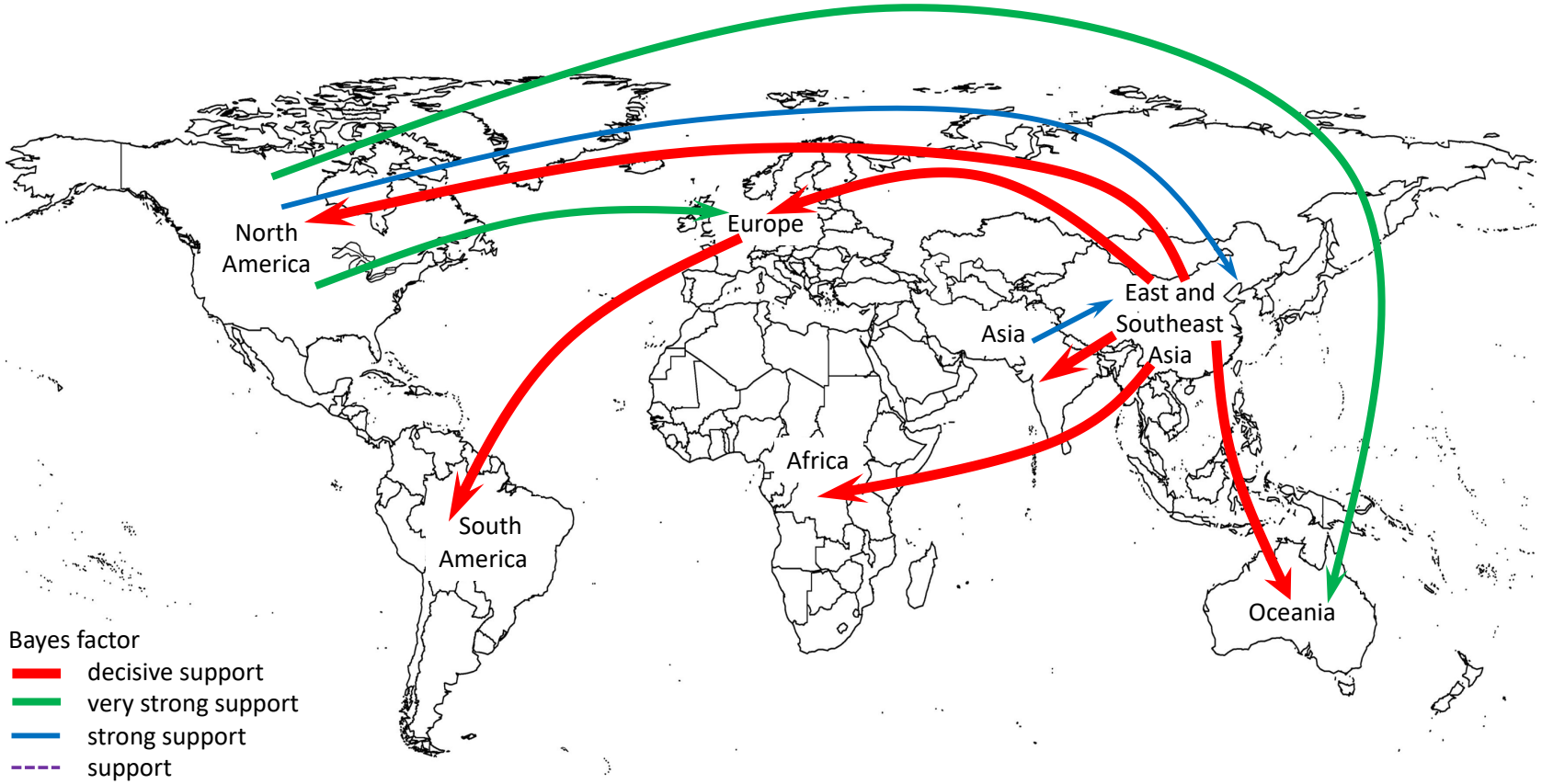


Figure 5.7: Global migration dynamics of influenza A(H1N1)pdm09 virus reconstructed using global virus sequences from geographical regions. Asymmetric migration pathways between location states were inferred for all global regions. Coloured line arrows indicate significant migration routes from one continent to another, while line thickness represents the degree of statistical support. Red arrowed lines are shown to indicate decisive migration routes with Bayes factor (BF) support ≥1000; green lines represent very strongly supported routes with 100≤BF<1000; blue lines indicate strongly supported routes 10≤BF<100; and purple dotted lines indicate supported routes with 3≤BF<10.

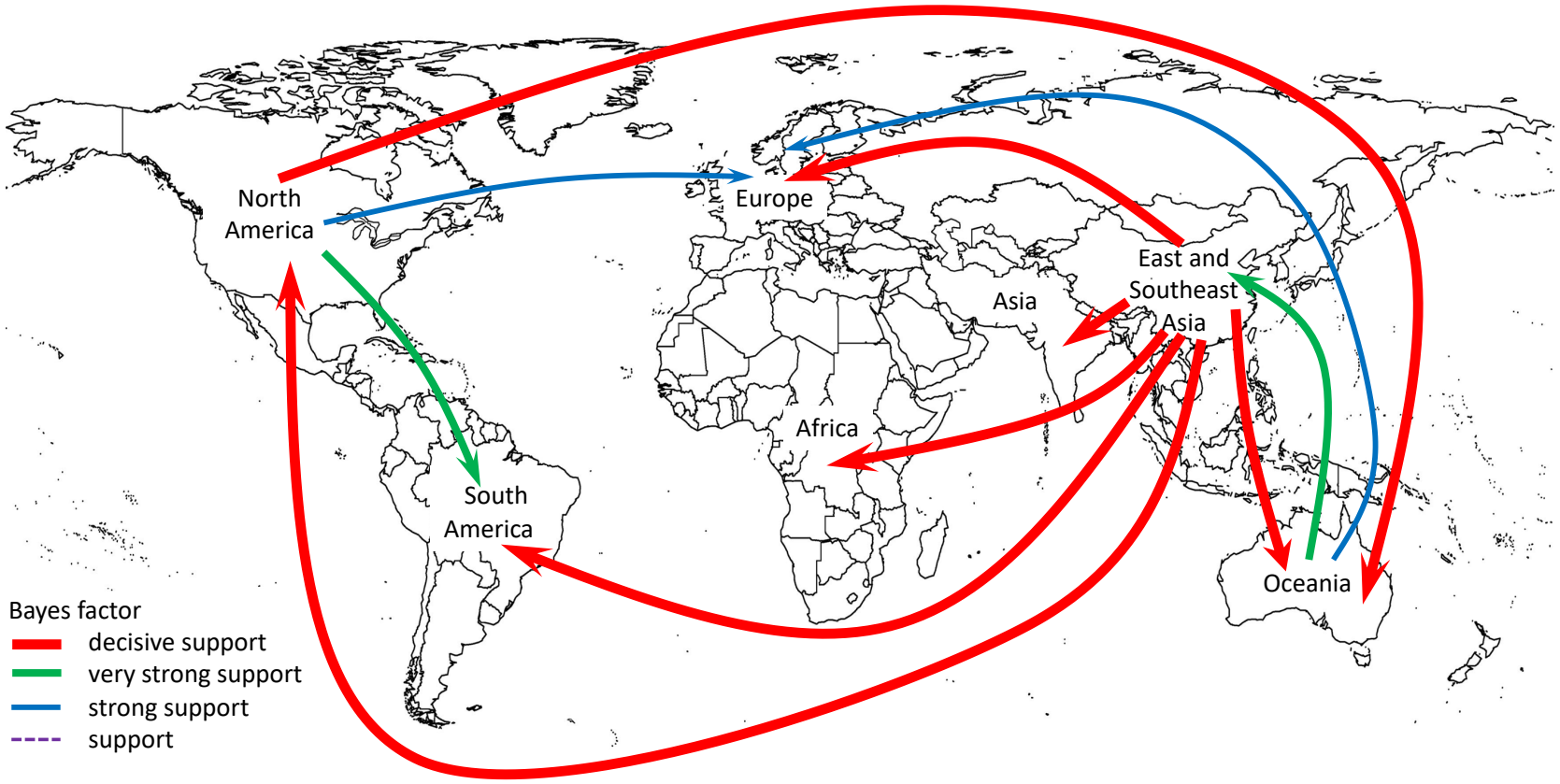


Figure 5.8: Global migration dynamics of influenza A(H3N2) virus reconstructed using global virus sequences from geographical regions. Asymmetric migration pathways between location states were inferred for all global regions. Coloured line arrows indicate significant migration routes from one continent to another, while line thickness represents the degree of statistical support. Red arrowed lines are shown to indicate decisive migration routes with Bayes factor (BF) support ≥1000; green lines represent very strongly supported routes with 100≤BF<1000; blue lines indicate strongly supported routes 10≤BF<100; and purple dotted lines indicate supported routes with 3≤BF<10.

The global geographic ancestries of A(H1N1)pdm09 and A(H3N2) viruses were inferred through ancestral state reconstruction of the geographical regions of internal nodes in the global virus phylogenies. The analysis was based on 7 discrete location states ("Africa", "Asia", "E-SE Asia", "Europe", "North America", "South America", and "Oceania"), which represent global virus transition states. For A(H1N1)pdm09 virus, global viruses coalesced to the trunk of the tree worldwide, with trunk viruses predominantly originating from North America in 2009-10, while E-SE Asia and Asia appeared to be the major source population in 2010-11, with predominance of E-SE Asia as source population (*Figure 5.9*). These findings are consistent with the apparent origins of A(H1N1)pdm09 viruses in the Americas in 2009, which seeded global viruses in 2009-10 and corroborate the findings of global A(H1N1)pdm09 virus migration dynamics in which significant migration pathways from E-SE Asia to multiple geographical regions were observed for the 2010-11 global epidemics (*Figure 5.7*). These observations suggest that the seeding of A(H1N1)pdm09 virus epidemics globally is driven by different geographical regions, which was initially predominated by North America due to virus origins in the Americas; seeding in subsequent epidemics following the pandemic period was then predominated by E-SE Asia.

For influenza A(H3N2) virus, a consistent pattern of global virus migration was observed in which viruses rapidly coalesced to the trunk of the tree worldwide (*Figure 5.9*), with trunk viruses mostly originating from E-SE Asia and India, consistent with the origins of the virus from E-SE Asia. These observations corroborate the findings of the global migration dynamics of A(H3N2) virus in which significant migration pathways from E-SE Asia to multiple geographical regions were observed. The coalescence of viruses to the trunk of the phylogenetic trees for A(H1N1)pdm09 virus was much slower than that for A(H3N2) virus, consistent with the hypothesis of rapid evolution of A(H3N2) virus compared with A(H1N1)pdm09 virus.

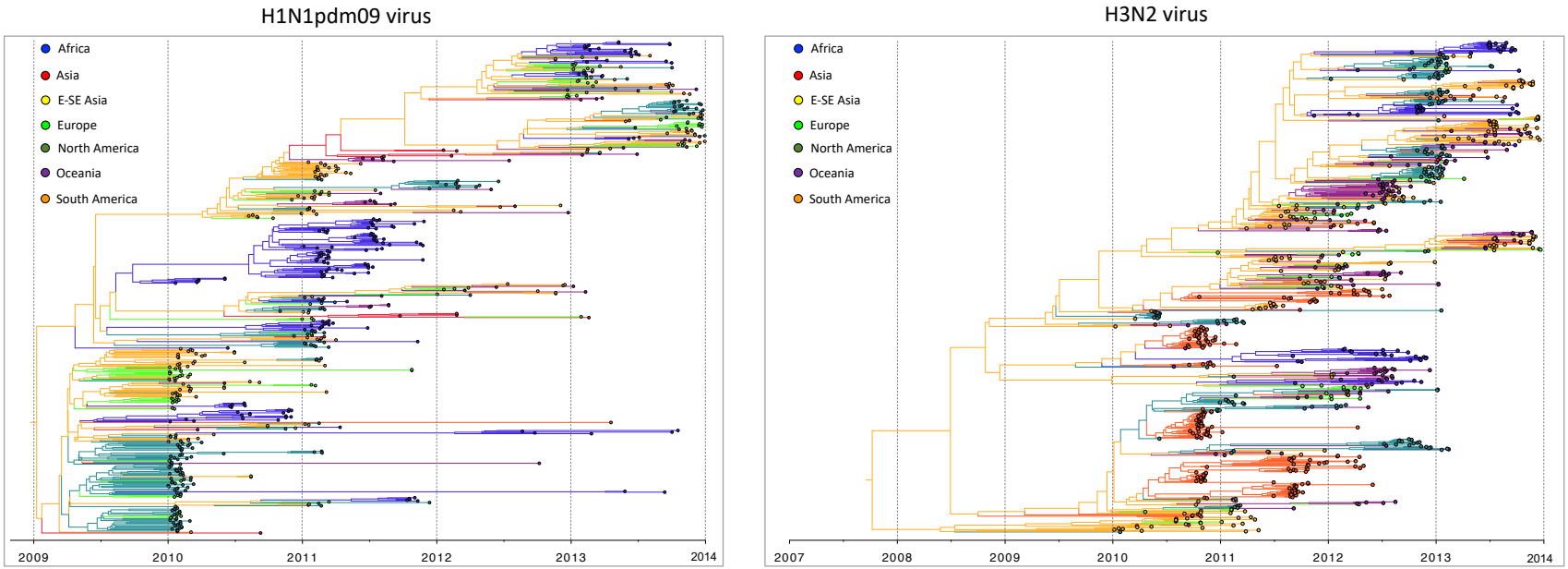


Figure 5.9: Time-resolved maximum-likelihood phylogenetic trees of African and global A(H1N1)pdm09 and A(H3N2) viruses. Branches and tips are coloured by geographic region of virus collection whereas internal branches are coloured by geographic region inferred by ancestral state reconstruction as shown in the legend.

5.4 Discussion

In this chapter, phylogeographical analysis of influenza A(H1N1)pdm09 and A(H3N2) viruses is reported, which provides a detailed overview of the circulation dynamics of the viruses in Africa. The results were obtained from genomic analysis of WGS data generated from Africa between 2010 and 2013, including contemporaneous global sequences generated within the same period. The analysis provides a finer resolution of the global migration dynamics of IAV in Africa immediately following the 2009-10 influenza A(H1N1)pdm09 virus pandemic. This novel work on understanding the role of Africa in the global migration dynamics of IAV was mainly conducted by reconstructing the phylogeographic history of the virus using Bayesian phylogeographical methods.

Phylogenetic analysis revealed extensive geographical mixing of A(H1N1)pdm09 and A(H3N2) viruses globally, which is associated with rapid and widespread mixing of viruses from Africa with those from multiple global regions, including in countries in Asia, E-SE Asia, Europe, North America, South America, and Oceania. Detailed examination of phylogenies of virus sequences from Africa provided evidence for the presence of strongly supported African sub-lineages for A(H1N1)pdm09 and A(H3N2) viruses, which consisted predominantly of strains from the same geographical regions. For example, for A(H1N1)pdm09 and A(H3N2) viruses, the African sub-lineages were observed for viruses in southern Africa (South Africa and Zambia) and western Africa (The Gambia and Mali), respectively, which is indicative of IAV spread between countries within same geographical regions in the continent. Additionally, viruses from different countries in Africa fell into some strongly supported multinational lineages for both viruses, for example, for A(H1N1)pdm09 virus (Kenya, South Africa, and Zambia) and for A(H3N2) virus (Kenya,

Uganda, South Africa and Zambia), which suggests possible intra-continental migration of A(H1N1)pdm09 virus within Africa.

To further explore the migration dynamics of IAV at a continental scale in the African continent, the phylogeography of A(H1N1)pdm09 and A(H3N2) viruses were reconstructed using Bayesian phylogeographic methods. First, at the continental scale of observation, IAV spread within the same geographical regions had significant migration pathways for A(H1N1)pdm09 virus and A(H3N2) virus. For example, significant migration pathways were observed in western Africa (from Mali to The Gambia) for A(H1N1)pdm09 virus whereas significant migration pathways were observed in western Africa (between The Gambia and Mali) for A(H3N2) virus, which represent widespread circulation of IAV within these regions. Overall, A(H3N2) virus exhibited more significant migration pathways compared with A(H1N1)pdm09 virus during the study period, which was dominated by global A(H3N2) virus circulation as observed from available epidemiological and global sequence data. In-depth investigation into the differences in global migration patterns between IAV and influenza B viruses have revealed more frequent A(H3N2) virus migration compared to A(H1N1)pdm09 and influenza B viruses (Bedford et al., 2015) that is associated with differences in rates of virus evolution, which is consistent with the findings in this study. Second, at the hemisphere scale of observation, significant migration pathways from the northern hemisphere to the southern hemisphere regions in Africa were observed for both viruses when the continent is partitioned into hemispheres at the Equator**.** These results support the concept of global migration of IAV that mainly involves the migration of viruses from temperate regions in the northern hemisphere to the tropical countries (Bedford et al., 2010).

Globally, significant migration pathways were observed for IAV. For A(H1N1)pdm09 virus, significant migration pathways from E-SE Asia into multiple geographical regions including

Africa, Asia, Europe, North America, and Oceania were observed. Additionally, significant migration pathways from North America to E-SE Asia, Europe, and Oceania were also observed. For A(H3N2) virus, significant migration pathways from E-SE Asia into all other geographical regions including Africa were observed. Additionally, significant migration pathways from North America to Europe, South America, and Oceania were observed. Taken together, these results suggest that the global seeding of epidemics of A(H1N1)pdm09 and A(H3N2) viruses is driven by different geographical regions, which also includes Africa, where E-SE Asia and North America are major transmission sources. By comparison, a greater global migration was observed for A(H3N2) virus compared to A(H1N1)pdm09 virus, which is consistent with greater global circulation of A(H3N2) viruses compared to A(H1N1)pdm09 virus (Bedford et al., 2010; Bedford et al., 2015).

The findings from this study support the notion that influenza viruses persist as temporally migrating metapopulations in which new virus strains can emerge in any geographical region, including Africa, with the location of the source population changing regularly (Bahl et al., 2011). In the model, virus migration into E-SE Asia occurs throughout the year with the migration contributing to local persistence of IAV in those regions, which seed global epidemics. Additionally, seasonal epidemics in temperate regions are seeded from a variety of geographical sources (Bahl et al., 2011). Here, for the first time, the role of Africa in the global migration dynamics of IAV is shown in which Africa is part of the global circulation of influenza viruses. The findings from this study support previous observations on the global migration dynamics of IAV, for example, for A(H3N2) virus whose global source region has been shown to be E-SE Asia and India (Bedford et al., 2010; Bedford et al., 2015; Rambaut et al., 2008; Russell et al., 2008). However, although geographically and temporally extensive, such studies were deficient in virus

sequences from Africa and other tropical and sub-tropical countries and failed to demonstrate the role of Africa in the global migration dynamics of IAV. Here, the role of Africa in the global migration dynamics of seasonal and emergent IAV has been demonstrated and underscores the importance of wider and deeper sampling from understudied tropical and sub-tropical regions notably Africa, India, and Latin America (Viboud et al., 2013) in order to reveal the underlying global migration dynamics of IAV.

Ancestral state reconstruction of the geographic ancestry in the global virus phylogenies revealed additional differences in the patterns of global migration of IAV. For A(H3N2) virus, global viruses rapidly coalesce to the trunk of the tree worldwide with trunk viruses mostly originating from E-SE Asia, which is consistent with origins of A(H3N2) viruses from E-SE Asia and India (Bedford et al., 2010; Bedford et al., 2015; Lemey et al., 2014; Russell et al., 2008). These observations corroborate the findings of the global migration dynamics of A(H3N2) viruses from this study in which significant migration pathways from E-SE Asia to all geographical regions were observed. On the other hand, the coalescence of the global A(H1N1)pdm09 viruses to the trunk of the tree worldwide was much slower compared to A(H3N2) viruses with trunk viruses predominantly originating from North America during the pandemic period 2009-10; migration pathways from E-SE Asia to multiple geographical regions were then observed for the 2011-13 global epidemics. The A(H1N1)pdm09 virus migration dynamics corroborate the findings from geographic ancestry in which seeding of A(H1N1)pdm09 virus epidemics globally is driven by multiple geographical locations, which was initially predominated by North America due to the apparent pandemic origins of the virus in the Americas (CDC, 2009; Garten et al., 2009) and subsequent seeding of global epidemics from E-SE Asia following the pandemic period.

Reconstruction of the past population dynamics revealed oscillating patterns in relative genetic diversity of A(H1N1)pdm09 virus globally after an initial rapid increase during the early pandemic spread, which broadly corresponded to the winter patterns in the northern and southern hemispheres (Su et al., 2015). The coalescent reconstruction of the outbreak in Kenya (see Chapter Four) revealed that the outbreak in the country was associated with relatively lower levels of relative genetic diversity and biannual epidemic peaks that corresponded to the seasonal outbreaks in the temperate regions; these patterns were similar to those observed in other tropical countries, for example, in India, Brazil and Singapore (Su et al., 2015). The biannual epidemic peaks in the tropical countries that corresponded to the seasonal outbreaks in temperate regions may be explained by coalescence of global A(H1N1)pdm09 viruses to the trunk of the global phylogeny in which trunk viruses predominantly originated from countries from North America. The temperate origins of A(H1N1)pdm09 virus phylogenies could then explain why A(H1N1)pdm09 viruses rapidly adapted to form seasonal epidemic patterns typical of seasonal influenza viruses, which initially broadly corresponded to the winter patterns in temperate regions (Su et al., 2015).

The paucity of sequence data from other sub-Saharan African countries limited our analysis of circulation dynamics and persistence patterns of IAV in the continent, which might have been useful to demonstrate intra-continental circulation of influenza viruses with more confidence. However, these findings have important implications for public health practice in the continent. For example, the rapid spread of A(H1N1)pdm09 virus throughout the continent, including in countries in eastern, western and southern Africa, provides evidence of how quickly influenza viruses can spread upon global emergence and introduction into a continent, which calls for continued strengthening of influenza surveillance efforts in the continent. There was evidence for regional circulation of influenza viruses in particular geographical regions, for example, in western

Africa (The Gambia and Mali) and in southern Africa (Zambia and South Africa); perhaps regional influenza surveillance efforts should be strengthened to complement national influenza surveillance programs in the different countries. Lastly, the rapid and widespread migration of global strains into Africa and widespread global mixing of viruses from Africa with viruses from both northern and southern hemisphere countries including Asia, Europe, North America, South America, and Oceania as reported in this study emphasize that vaccine recommendations in the two hemispheres need well distributed, widespread global influenza A(H1N1)pdm09 virus and A(H3N2) virus sampling from as many localities as possible.

CHAPTER SIX

6 Overall Discussion

6.1 Introduction

The global surveillance of human influenza viruses through GISRS and NICs (World Health Organization, 2017) has resulted in the generation of a uniquely extensive collection of geographically and temporally comprehensive virus sequence data, which has provided an opportunity to explore the global migration dynamics of influenza viruses (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Kosakovsky Pond et al., 2010; Rambaut et al., 2008; Russell et al., 2008). Most of the analyses on the drivers behind the global migration of influenza viruses have aimed at investigating the global source population of influenza viruses with several hypotheses being proposed to describe these patterns mainly based on phylogenetic analysis of virus sequence data (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Rambaut et al., 2008). However, these have not completely described the global migration patterns of the viruses. A more complete understanding of the global migration dynamics of influenza viruses requires deeper and wider sampling from understudied tropical and sub-tropical regions (Viboud et al., 2013). Because of the insufficient spatiotemporally representative virus sequence data from tropical and sub-tropical African countries, especially from sub-Saharan Africa, relatively little is known about the possible role the region plays in the global migration of influenza viruses (Ng and Gordon, 2015; Viboud et al., 2013). The studies on the global circulation of influenza viruses acknowledged the lack of virus sequence data from Africa, South and Central Asia, and South America in their inferences of the spread of the viruses as a major study limitation (Bahl et al., 2011; Bedford et al., 2010; Bedford et al., 2015; Kosakovsky Pond et al., 2010; Russell et al., 2008).

In this study, I successfully transferred an influenza virus WGS protocol from USA CDC Influenza Genomics team, and established it locally at Kilifi, coastal Kenya, to be used on an Illumina NGS platform. Using this method, I processed and assembled a total of 549 new influenza virus genomes from archived positive samples collected between 2009 and 2018. These samples had been collected at different scales of observation with a variety of study designs. An integrated approach was then henceforth undertaken using A(H1N1)pdm09 virus and A(H3N2) virus WGS data, patient clinical and demographic profiles, and stochastic models of transmission of influenza viruses to understand: (i) how novel influenza virus strains are introduced and spread into a local community in Kilifi, countrywide around Kenya, and continentwide across Africa, and (ii) the patterns and drivers of spread of influenza viruses across geographically defined regions, whether local, national, continental or global.

6.2 Key Research Findings

The key findings from this thesis project are presented hereafter under each of the 3 major analyses.

6.2.1 Phylogeography of Influenza A(H3N2) Virus in Kilifi, Kenya, 2015-2016

Several prospective, hospital- and community-based influenza surveillance cohorts exist in multiple regions of Kenya, which provide a unique opportunity to examine the molecular epidemiology of seasonal influenza viruses within the country. To better understand the patterns of spread of influenza viruses in a rural community in coastal Kenya and the origins of viruses that seed epidemics at the local community, an analysis of a set of 58 WGS data sampled from 9 outpatient health facilities between December 2015 and December 2016 from Kilifi, Kenya along with 1,571 contemporaneous global WGS data was conducted to describe the local patterns of spread of A(H3N2) virus and the source population of virus introductions into Kilifi, Kenya.

The following key findings were made:

1. The year-round circulation of A(H3N2) virus in the coastal Kenya region was characterized by co-circulation of multiple virus clades and clusters, the epidemic season initiated by independent virus introductions into the local community; each introduction commonly circulated in multiple locations in a relatively short period of time. Following introduction, the viruses exhibited extensive local spread throughout the community, with migration of virus strains from more populous to less populous locations or between locations in proximity, which was associated with predominantly local evolution in a majority of the locations.
2. Existence of strong spatial clustering patterns of A(H3N2) virus in majority of the locations, which was consistent with semi-localized virus epidemics in the community, although with migration between localities. The strongest spatial structure existed in the most populous locations, which was associated with rapid and widespread virus spread whereas weaker spatial clustering patterns in the less populous locations was likely associated with limited virus spread.
3. Extensive global A(H3N2) virus migration with widespread mixing of viruses from the local community with those from multiple global regions, which was consistent with those of studies from other countries that showed regular introductions of new virus lineages into specific locales and seeding of local seasonal epidemics rather than inter-seasonal persistence of lineages. Globally, annual influenza epidemics are associated with multiple introductions of influenza viruses into different locales that then establish transmission chains across the country as observed in this study. Additionally, existence of some strongly supported multinational sub-lineages consisting of strains from eastern, central

and southern African countries suggested considerable A(H3N2) virus migration throughout the African continent.

6.2.2 Phylogeography of Influenza A(H1N1)pdm09 Virus in Kenya, 2009-2018

The first laboratory-confirmed case of influenza A(H1N1)pdm09 virus in Kenya was reported on June 29, 2009 with sentinel surveillance activities by the Kenyan MoPHS reporting 4 parallel introductions of A(H1N1)pdm09 virus into Kenya during the pandemic period in 2009. To better understand the spatiotemporal patterns of spread of A(H1N1)pdm09 virus in Kenya since its introduction into the local population, an analysis of the evolution and spread of the virus in the country was conducted using 383 A(H1N1)pdm09 virus WGS data sampled between 2009 and 2018 from 7 sentinel surveillance sites in Kenya along with 1,587 publicly available global WGS data.

The following key findings were made:

1. Oscillating patterns in relative genetic diversity of A(H1N1)pdm09 virus in Kenya after an initial rapid increase during the early pandemic spread, which were associated with relatively lower levels of relative genetic diversity and biannual epidemic peaks that corresponded to the seasonal outbreaks and winter patterns in the northern and southern hemispheres. These findings suggest that after its global emergence, A(H1N1)pdm09 virus rapidly adapted to form seasonal epidemic patterns typical of seasonal influenza viruses in all countries including Kenya. The relative genetic diversity of A(H1N1)pdm09 virus in Kenya peaked in December 2009 despite the earliest reports of the virus from the country starting in late June 2009, which suggests that the initial outbreak was limited in spread and duration.

2. The seasonal patterns of A(H1N1)pdm09 virus took longer to be established in Kenya and showed little or no virus activity is some years, which corresponded to local epidemics being dominated by A(H3N2) and influenza B viruses. Kenya experienced some variation in A(H1N1)pdm09 virus seasonal intensity with smaller epidemics observed in mid-2010, mid-2011, and mid-2013 while virus diversity was markedly reduced in 2012-2013 and 2016-2017. The country also experienced limited A(H1N1)pdm09 virus activity in 2012, 2013, and 2016, which corresponded with higher incidences of A(H3N2) and influenza B viruses.
3. Extensive global migration of A(H1N1)pdm09 virus following its emergence with rapid and widespread mixing of Kenyan viruses with those from multiple global regions, which was associated with multiple A(H1N1)pdm09 virus introductions into Kenya that then established transmission chains within the country. These findings are consistent with those of studies from other countries, which showed regular introductions of new virus lineages and seeding of local seasonal epidemics. At the countrywide level, migration of A(H1N1)pdm09 virus was predominantly characterized by virus transitions from multiple locations to multiple destinations within the country and between locations in proximity. Therefore, virus persistence in Kenya might be modulated by frequent A(H1N1)pdm09 virus introductions from outside the country and virus migration between locations in proximity.
4. Strains from Kenya fell into some strongly supported multinational lineages with strains from eastern, central and southern Africa, which suggests possible A(H1N1)pdm09 virus migration throughout the African continent. Furthermore, viruses from the continent fell into some regional lineages consisting of viruses from western Africa, central Africa and

southern Africa, which suggests regional patterns of migration of A(H1N1)pdm09 virus in Africa.

6.2.3 Phylogeography of Influenza A(H1N1)pdm09 and A(H3N2) Viruses in Africa, 2011-2013

Analysis of WGS data of influenza viruses from Kenya and additional contemporaneous WGS data from Africa and other global regions revealed extensive geographical mixing of A(H1N1)pdm09 and A(H3N2) viruses globally, which was associated with widespread mixing of viruses from Kenya with those from multiple global regions, including in countries in Africa, Asia, E-SE Asia, Europe, North America, South America, and Oceania. Additionally, IAV strains from Kenya formed strongly supported multinational lineages with strains from multiple African regions, which suggests possible intra-continental migration of A(H1N1)pdm09 and A(H3N2) viruses. Viruses from Africa also formed some strongly supported regional lineages consisting of viruses from eastern Africa, western Africa, central Africa and southern Africa, which suggests regional patterns of IAV migration within the continent. However, the paucity of virus sequence data from Africa, especially from sub-Saharan African countries, limited the analysis of virus migration dynamics and persistence patterns in the continent, which might have been useful in demonstrating an intra-continental migration dynamic. The paucity of virus sequence data also limited the analysis of the role of the continent in the global migration of influenza viruses. For this analysis, additional WGS data of IAV from Africa was analyzed to re-examine the intra-continental migration dynamics of A(H1N1)pdm09 and A(H3N2) viruses in Africa and the role of the continent in the global circulation of influenza viruses.

The following key findings were made:

1. Presence of strongly supported African sub-lineages for A(H1N1)pdm09 and A(H3N2) viruses, which consisted predominantly of strains from the same geographical regions, for example, southern and western Africa, which is indicative of virus spread between countries within the same geographical regions in the continent. Additionally, viruses from different countries in Africa fell into some strongly supported multinational lineages for IAV, for example, for A(H1N1)pdm09 virus (Kenya, South Africa, and Zambia) and A(H3N2) virus (Kenya, Uganda, South Africa, and Zambia), which suggests possible intra-continental spread of IAV within Africa. Bayesian methods corroborated these findings and revealed significant migration pathways for A(H1N1)pdm09 and A(H3N2) viruses within the same geographical regions. At the hemisphere level of observation, significant migration pathways for A(H1N1)pdm09 and A(H3N2) viruses were observed from the northern hemisphere to the southern hemisphere regions.
2. Globally, significant migration pathways from E-SE Asia and North America into multiple geographical regions were observed for A(H1N1)pdm09 and A(H3N2) viruses. Furthermore, significant migration pathways from multiple geographical regions to multiple geographical destinations, which also includes Africa, were observed. Taken together, these results suggest that the seeding of A(H1N1)pdm09 virus and A(H3N2) virus epidemics globally is driven by different geographical locations that also includes Africa, where E-SE Asia and North America are the major sources of transmission. A greater global migration was observed for A(H3N2) virus compared to A(H1N1)pdm09 virus that is consistent with greater global circulation of A(H3N2) virus. The findings from this study support the notion that influenza viruses persist as temporally structured migrating metapopulations in which new virus strains can emerge in any geographical region,

including in Africa, with the location of the source population changing regularly. In addition, these findings support previous observations on the global migration dynamics of IAV in which E-SE Asia and India have been shown to be the global source region for influenza viruses.

3. Inference of geographic ancestry revealed differences in global patterns of migration of A(H1N1)pdm09 and A(H3N2) viruses. For A(H3N2) virus, global viruses rapidly coalesced to the trunk of the tree worldwide, with trunk viruses mostly originating from E-SE Asia, which corroborated the findings of the global migration of A(H3N2) virus that showed significant migration pathways from E-SE Asia to multiple geographical regions consistent with origins of A(H3N2) viruses from E-SE Asia and India. For A(H1N1)pdm09 virus, coalescence of global viruses to the trunk of the tree worldwide was much slower compared to A(H3N2) virus, which is consistent with findings from other studies. Trunk viruses predominantly originated from North America during the pandemic period 2009-2010 followed by origins from E-SE Asia in 2011-2013 epidemics. These findings corroborated the apparent pandemic origins of A(H1N1)pdm09 virus in the Americas in which trunk viruses predominantly originated from North America and subsequent seeding of global epidemics by E-SE Asia following the pandemic period.

6.3 Study Limitations

While all the study objectives were addressed, the small sample sizes from Kilifi and Kenya, for the community and countrywide studies, respectively and the paucity of virus sequence data from sub-Saharan Africa for the continentwide study was a constraint on the analysis of spread and persistence of influenza viruses across these geographically defined regions. Additionally, the poor representation of locations across these geographically defined regions could potentially have

hidden the routes of transmission of influenza viruses in the regions. For example, although phylogenetic analysis revealed that multiple introductions of A(H3N2) virus into Kilifi occurred, with the epidemic season initiated by at least 3 independent virus introductions, the small sample size and poor representation of the KHDSS locations may have limited the spatiotemporal inference of viral introductions into Kilifi and the local patterns of spread of A(H3N2) virus. Additionally, the conclusion of virus spread between Kilifi, Kenya and its neighbor countries in East Africa was uncertain due to the small number of sequences from the neighbor countries and the poor representation of locations in the neighbor countries. For the countrywide study of A(H1N1)pdm09 virus, all Kenyan source lineages that seed peripheral locations in the country may not have been sampled over the study period and important locations of virus migration within the country may have been poorly represented. Therefore, the suggestion of possible virus migration into and out of Kenyan locations outside the main air-transport hub of Nairobi, which is based on countrywide mixing of viruses between all sampled locations must be interpreted carefully. The paucity of virus sequence data from sub-Saharan Africa and the poor representation of sub-Saharan African countries constrained the analysis of virus migration and patterns of persistence in the continent, which might have been useful to adequately demonstrate intra-continental spread of A(H1N1)pdm09 and A(H3N2) viruses.

Although the origins and spread of A(H1N1)pdm09 and A(H3N2) viruses across the geographically defined regions were reconstructed using phylogeographical methods, which employ stochastic models of transmission of influenza viruses, several shortcomings were inherent in the Bayesian inference models. First, the analyses were very slow for larger datasets due to the large number of parameters that were estimated in the Bayesian models, which limited the number of parameters in the models. Additionally, the number of distinct states that could be modelled was

limited due to the slow nature of the models for larger datasets whereas the biased number of sequences per trait, where there were few sequences for some traits, biased rates matrix inference. Therefore, locations were aggregated into larger regions, for example, into continents for most of the Bayesian inference models, even though more finely resolved locations such as countries, cities, and towns were available for most of the sequences in this study. Second, the discrete Bayesian inference models that were employed generally estimate rates of virus migration from the data, thus only infer observed locations; this excluded possible intermediate states that had not been sampled from the available sequence data. Lastly, there was an effect of sampling bias on phylogeographic reconstructions due to the biased distribution of global virus genomes as well as lack of sufficient strategies to mitigate the bias incorporated within the Bayesian model parameters.

Alternative models are being explored for phylogeographical reconstruction using the available sequence data to overcome the shortcomings inherent in the Bayesian models used in this study and to verify the findings from the Bayesian inferences. For example, a maximum-likelihood evolutionary model inference method (Hadfield et al., 2018; Sagulenko et al., 2018) and a parsimony-based approach (Reimering et al., 2020) for phylogeographic reconstruction are being evaluated. The maximum-likelihood inference method incorporates ancestral state reconstruction of discrete states such as country or region of isolation allowing inference of the most likely transmission events (Sagulenko et al., 2018) whereas the parsimony-based approach uses a unique algorithm to identify internal locations, which minimizes the distances along the phylogenetic tree and allows for the use of fine-grained locations and inference of intermediate locations (Reimering et al., 2020). Using these approaches, it is possible to: (i) use finely resolved locations such as countries, cities, and towns that are available for most of the virus sequences; (ii) infer intermediate

locations; and (iii) increase the number of distinct states that can be modelled in the analyses. This work is part of ongoing analyses for the manuscript drafts listed in Chapter One, section 1.16.2.

6.4 Thesis Summary

This project established a local influenza WGS protocol in coastal Kenya and significantly increased available WGS data from Africa. Phylogeographical analyses revealed that influenza virus epidemics at the local community in coastal Kenya were initiated by multiple independent introductions into the community, with each introduction commonly circulating in multiple locations in a relatively short period of time. For Kenya countrywide, virus migration was predominantly characterized by migration from multiple locations to multiple destinations within the country and between locations in proximity. Thus, countrywide persistence of influenza viruses might be modulated by frequent virus introductions from outside Kenya and virus spread between locations in proximity. Community and countrywide strains fell into strongly supported African sub-lineages that predominantly consisted of strains from the same geographical regions indicative of virus spread between countries within the same geographical regions in Africa. Additionally, virus strains from Africa fell into some strongly supported multinational lineages, which suggests possible intra-continental spread of influenza viruses within Africa that exhibited a significant northern hemisphere to southern hemisphere migration. On a global scale, significant migration pathways from multiple geographical regions to multiple geographical destinations, including Africa, was observed, which suggests that the seeding of influenza virus epidemics globally is driven by different geographical locations that also includes Africa, where E-SE Asia acts as the major source of transmission. However, a greater global migration was observed for A(H3N2) virus compared to A(H1N1)pdm09 virus consistent with greater global migration of A(H3N2) virus. The findings from this study support the notion that influenza viruses persist as temporally

structured migrating metapopulations in which new virus strains can emerge in any geographical region, including in Africa, with the location of the source population changing regularly.

REFERENCES

Amato-Gauci, A., Zucs, P., Snacken, R., Ciancio, B., Lopez, V., Broberg, E., Penttinen, P., Nicoll, A., on behalf of the European Influenza Surveillance Network , c. (2011) 'Surveillance trends of the 2009 influenza A(H1N1) pandemic in Europe'. *Eurosurveillance 16*, 19903.

Au, K. F., Underwood, J. G., Lee, L., Wong, W. H. (2012) 'Improving PacBio Long Read Accuracy by Short Read Alignment'. *PLOS ONE 7*, e46679.

Baele, G., Suchard, M. A., Rambaut, A., Lemey, P. (2017) 'Emerging Concepts of Data Integration in Pathogen Phylodynamics'. *Syst Biol 66*, e47-e65.

Bahl, J., Nelson, M. I., Chan, K. H., Chen, R., Vijaykrishna, D., Halpin, R. A., Stockwell, T. B., Lin, X., Wentworth, D. E., Ghedin, E., Guan, Y., Peiris, J. S., Riley, S., Rambaut, A., Holmes, E. C., Smith, G. J. (2011) 'Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans'. *Proc Natl Acad Sci U S A 108*, 19359-19364.

Baillie, G. J., Galiano, M., Agapow, P. M., Myers, R., Chiam, R., Gall, A., Palser, A. L., Watson, S. J., Hedge, J., Underwood, A., Platt, S., McLean, E., Pebody, R. G., Rambaut, A., Green, J., Daniels, R., Pybus, O. G., Kellam, P., Zambon, M. (2012) 'Evolutionary dynamics of local pandemic H1N1/2009 influenza virus lineages revealed by whole-genome analysis'. *J Virol 86*, 11-18.

Barberis, I., Martini, M., Iavarone, F., Orsi, A. (2016a) 'Available influenza vaccines: immunization strategies, history and new tools for fighting the disease'. *J Prev Med Hyg 57*, E41-E46.

Barberis, I., Myles, P., Ault, S. K., Bragazzi, N. L., Martini, M. (2016b) 'History and evolution of influenza control through vaccination: from the first monovalent vaccine to universal vaccines'. *J Prev Med Hyg 57*, E115-E120.

Bedford, T., Cobey, S., Beerli, P., Pascual, M. (2010) 'Global migration dynamics underlie evolution and persistence of human influenza A (H3N2)'. *PLoS Pathog 6*, e1000918.

Bedford, T., Huddleston, J., Potter, B., Neher, R. A. (2019) 'Seasonal infuenza circulation patterns and projections for September 2019 to September 2020'.

Bedford, T., Riley, S., Barr, I. G., Broor, S., Chadha, M., Cox, N. J., Daniels, R. S., Gunasekaran, C. P., Hurt, A. C., Kelso, A., Klimov, A., Lewis, N. S., Li, X., McCauley, J. W., Odagiri, T., Potdar, V., Rambaut, A., Shu, Y., Skepner, E., Smith, D. J., Suchard, M. A., Tashiro, M., Wang, D., Xu, X., Lemey, P., Russell, C. A. (2015) 'Global circulation patterns of seasonal influenza viruses vary with antigenic drift'. *Nature 523*, 217-220.

Bedford, T., Suchard, M. A., Lemey, P., Dudas, G., Gregory, V., Hay, A. J., McCauley, J. W., Russell, C. A., Smith, D. J., Rambaut, A. (2014) 'Integrating influenza antigenic dynamics with molecular evolution'. *eLife 3*.

Belanov, S. S., Bychkov, D., Benner, C., Ripatti, S., Ojala, T., Kankainen, M., Kai Lee, H., Wei-Tze Tang, J., Kainov, D. E. (2015) 'Genome-Wide Analysis of Evolutionary Markers of Human Influenza A(H1N1)pdm09 and A(H3N2) Viruses May Guide Selection of Vaccine Strain Candidates'. *Genome Biol Evol 7*, 3472-3483.

Bielejec, F., Baele, G., Vrancken, B., Suchard, M. A., Rambaut, A., Lemey, P. (2016) 'SpreaD3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes'. *Mol Biol Evol 33*, 2167-2169.

Bliven, K. A., Maurelli, A. T. (2016) 'Evolution of Bacterial Pathogens Within the Human Host'. *Microbiol Spectr 4*.

Bloomquist, E. W., Lemey, P., Suchard, M. A. (2010) 'Three roads diverged? Routes to phylogeographic inference'. *Trends Ecol Evol 25*, 626-632.

Bodewes, R., Morick, D., de Mutsert, G., Osinga, N., Bestebroer, T., van der Vliet, S., Smits, S. L., Kuiken, T., Rimmelzwaan, G. F., Fouchier, R. A., Osterhaus, A. D. (2013) 'Recurring influenza B virus infections in seals'. *Emerg Infect Dis 19*, 511-512.

Borges, V., Pinheiro, M., Pechirra, P., Guiomar, R., Gomes, J. P. (2018) 'INSaFLU: an automated open web-based bioinformatics suite "from-reads" for influenza whole-genome-sequencing-based surveillance'. *Genome Med 10*, 46.

Bouvier, N. M., Palese, P. (2008) 'The Biology of Influenza Viruses'. *Vaccines 26 (Suppl 4)*, D49-D53.

Breiman, R. F., Cosmas, L., Njenga, M., Williamson, J., Mott, J. A., Katz, M. A., Erdman, D. D., Schneider, E., Oberste, M., Neatherlin, J. C., Njuguna, H., Ondari, D. M., Odero, K., Okoth, G. O., Olack, B., Wamola, N., Montgomery, J. M., Fields, B. S., Feikin, D. R. (2015) 'Severe acute respiratory infection in children in a densely populated urban slum in Kenya, 2007-2011'. *BMC Infect Dis 15*, 95.

Byarugaba, D. K., Erima, B., Millard, M., Kibuuka, H., Lkwago, L., Bwogi, J., Mimbe, D., Kiconco, J. B., Tugume, T., Mworozi, E. A., Turner, J., McKenzie, P. P., Webby, R. R., Webster, R. G., Foret, C., Ducatez, M. F., Coldren, R., Wabwire-Mangen, F., Krauss, S. (2016) 'Whole-genome analysis of influenza A(H1N1)pdm09 viruses isolated in Uganda from 2009 to 2011'. *Influenza Other Respir Viruses 10*, 486-492.

CDC. 'FluView 2009-2010' [Online]. Available: https://www.cdc.gov/flu/weekly/weeklyarchives2009-2010/09-10summary.htm [Accessed].

CDC (2009) 'Outbreak of swine-origin influenza A (H1N1) virus infection–Mexico, March–April 2009'. *MMWR Morb Mortal Wkly Rep 58*, 467-470.

CDC (2009a) 'Introduction and transmission of 2009 pandemic influenza A (H1N1) virus—Kenya, June–July 2009'. *MMWR Morb Mortal Wkly Rep 58*, 1143-1146.

CDC (2009b) 'Swine influenza A (H1N1) infection in two children-Southern California, March–April 2009'. *MMWR Morb Mortal Wkly Rep 58*, 400-402.

Cheng, X., Tan, Y., He, M., Lam, T. T.-Y., Lu, X., Viboud, C., He, J., Zhang, S., Lu, J., Wu, C., Fang, S., Wang, X., Xie, X., Ma, H., Nelson, M. I., Kung, H.-f., Holmes, E. C., Cheng, J. (2013) 'Epidemiological Dynamics and Phylogeography of Influenza Virus in Southern China'. *The Journal of Infectious Diseases 207*, 106-114.

Chiapponi, C., Faccini, S., De Mattia, A., Baioni, L., Barbieri, I., Rosignoli, C., Nigrelli, A., Foni, E. (2016) 'Detection of Influenza D Virus among Swine and Cattle, Italy'. *Emerging infectious diseases 22*, 352-354.

Collin, E. A., Sheng, Z., Lang, Y., Ma, W., Hause, B. M., Li, F. (2015) 'Cocirculation of Two Distinct Genetic and Antigenic Lineages of Proposed Influenza D Virus in Cattle'. *Journal of Virology 89*, 1036-1042.

Connor, T. R., Loman, N. J., Thompson, S., Smith, A., Southgate, J., Poplawski, R., Bull, M. J., Richardson, E., Ismail, M., Thompson, S. E., Kitchen, C., Guest, M., Bakke, M., Sheppard, S. K., Pallen, M. J. (2016) 'CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community'. *Microb Genom 2*, e000086.

Crawley, J., Prosperi, C., Baggett, H. C., Brooks, W. A., Deloria Knoll, M., Hammitt, L. L., Howie, S. R. C., Kotloff, K. L., Levine, O. S., Madhi, S. A., Murdoch, D. R., O'Brien, K. L., Thea, D. M., Awori, J. O., Bunthi, C., DeLuca, A. N., Driscoll, A. J., Ebruke, B. E., Goswami, D., Hidgon, M. M., Karron, R. A., Kazungu, S., Kourouma, N., Mackenzie, G., Moore, D. P., Mudau, A., Mwale, M., Nahar, K., Park, D. E., Piralam, B., Seidenberg, P., Sylla, M., Feikin, D. R., Scott, J. A. G., O'Brien, K. L., Levine, O. S., Knoll, M. D., Feikin, D. R., DeLuca, A. N., Driscoll, A. J., Fancourt, N., Fu, W., Hammitt, L. L., Higdon, M. M., Kagucia, E. W., Karron, R. A., Li, M., Park, D. E., Prosperi, C., Wu, Z., Zeger, S. L., Watson, N. L., Crawley, J., Murdoch, D. R., Brooks, W. A., Endtz, H. P., Zaman, K., Goswami, D., Hossain, L., Jahan, Y., Ashraf, H., Howie, S. R. C., Ebruke, B. E., Antonio, M., McLellan, J., Machuka, E., Shamsul, A., Zaman, S. M. A., Mackenzie, G., Scott, J. A. G., Awori, J. O., Morpeth, S. C., Kamau, A., Kazungu, S., Kotloff, K. L., Tapia, M. D., Sow, S. O., Sylla, M., Tamboura, B., Onwuchekwa, U., Kourouma, N., Toure, A., Madhi, S. A., Moore, D. P., Adrian, P. V., Baillie, V. L., Kuwanda, L., Mudau, A., Groome, M. J., Baggett, H. C., Thamthitiwat, S., Maloney, S. A., Bunthi, C., Rhodes, J., Sawatwong, P., Akarasewi, P., Thea, D. M., Mwananyanda, L., Chipeta, J., Seidenberg, P., Mwansa, J., wa Somwe, S., Kwenda, G. (2017) 'Standardization of Clinical Assessment and Sample Collection Across All PERCH Study Sites'. *Clinical Infectious Diseases 64*, S228-S237.

Danecek, P., Auton, A., Abecasis, G., Albers, C. A., Banks, E., DePristo, M. A., Handsaker, R. E., Lunter, G., Marth, G. T., Sherry, S. T., McVean, G., Durbin, R., Genomes Project Analysis, G. (2011) 'The variant call format and VCFtools'. *Bioinformatics 27*, 2156-2158.

Dawood, F. S., Iuliano, A. D., Reed, C., Meltzer, M. I., Shay, D. K., Cheng, P.-Y., Bandaranayake, D., Breiman, R. F., Brooks, W. A., Buchy, P., Feikin, D. R., Fowler, K. B., Gordon, A., Hien, N. T., Horby, P., Huang, Q. S., Katz, M. A., Krishnan, A., Lal, R., Montgomery, J. M., Mølbak, K., Pebody, R., Presanis, A. M., Razuri, H., Steens, A., Tinoco, Y. O., Wallinga, J., Yu, H., Vong, S.,

Bresee, J., Widdowson, M.-A. (2012) 'Estimated global mortality associated with the first 12 months of 2009 pandemic influenza A H1N1 virus circulation: a modelling study'. *The Lancet Infectious Diseases 12*, 687-695.

Dawood, F. S., Jain, S., Finelli, L., Shaw, M. W., Lindstrom, S., Garten, R. J., Gubareva, L. V., Xu, X., Bridges, C. B., Uyeki, T. M., Team, N. S.-O. I. A. V. I. (2009) 'Emergence of a Novel Swine-Origin Influenza A (H1N1) Virus in Humans'. *New England Journal of Medicine 360*, 2605-2615.

Deloria-Knoll, M., Feikin, D. R., Scott, J. A., O'Brien, K. L., DeLuca, A. N., Driscoll, A. J., Levine, O. S., Pneumonia Methods Working, G. (2012) 'Identification and selection of cases and controls in the Pneumonia Etiology Research for Child Health project'. *Clin Infect Dis 54 Suppl 2*, S117-123.

Deng, Y. M., Spirason, N., Iannello, P., Jelley, L., Lau, H., Barr, I. G. (2015) 'A simplified Sanger sequencing method for full genome sequencing of multiple subtypes of human influenza A viruses'. *J Clin Virol 68*, 43-48.

Dia, N., Ndiaye, M. N., Monteiro Mde, L., Koivogui, L., Bara, M. O., Diop, O. M. (2013) 'A subregional analysis of epidemiologic and genetic characteristics of influenza A(H1N1)pdm09 in Africa: Senegal, Cape Verde, Mauritania, and Guinea, 2009-2010'. *Am J Trop Med Hyg 88*, 946-953.

Driscoll, A. J., Karron, R. A., Morpeth, S. C., Bhat, N., Levine, O. S., Baggett, H. C., Brooks, W. A., Feikin, D. R., Hammitt, L. L., Howie, S. R. C., Knoll, M. D., Kotloff, K. L., Madhi, S. A., Scott, J. A. G., Thea, D. M., Adrian, P. V., Ahmed, D., Alam, M., Anderson, T. P., Antonio, M., Baillie, V. L., Dione, M., Endtz, H. P., Gitahi, C., Karani, A., Kwenda, G., Maiga, A. A., McClellan, J., Mitchell, J. L., Morailane, P., Mugo, D., Mwaba, J., Mwansa, J., Mwarumba, S., Nyongesa, S., Panchalingam, S., Rahman, M., Sawatwong, P., Tamboura, B., Toure, A., Whistler, T., O'Brien, K. L., Murdoch, D. R. (2017) 'Standardization of Laboratory Methods for the PERCH Study'. *Clinical Infectious Diseases 64*, S245-S252.

Dutch, R. E., Ma, W., García-Sastre, A., Schwemmle, M. (2015) 'Expected and Unexpected Features of the Newly Discovered Bat Influenza A-like Viruses'. *PLOS Pathogens 11*, e1004819.

Economist, T. 2013. 'More than minerals' [Online]. Available: https://www.economist.com/middle-east-and-africa/2013/03/23/more-than-minerals [Accessed].

Eisler, D., Fornika, D., Tindale, L. C., Chan, T., Sabaiduc, S., Hickman, R., Chambers, C., Krajden, M., Skowronski, D. M., Jassem, A., Hsiao, W. (2020) 'Influenza Classification Suite: An automated Galaxy workflow for rapid influenza sequence analysis'. *Influenza and Other Respiratory Viruses 14*, 358-362.

Emukule, G. O., Khagayi, S., McMorrow, M. L., Ochola, R., Otieno, N., Widdowson, M. A., Ochieng, M., Feikin, D. R., Katz, M. A., Mott, J. A. (2014) 'The burden of influenza and RSV among inpatients and outpatients in rural western Kenya, 2009-2012'. *PLoS One 9*, e105543.

Emukule, G. O., Mott, J. A., Spreeuwenberg, P., Viboud, C., Commanday, A., Muthoka, P., Munywoki, P. K., Nokes, D. J., van der Velden, K., Paget, J. W. (2016) 'Influenza activity in Kenya, 2007-2013: timing, association with climatic factors, and implications for vaccination campaigns'. *Influenza and Other Respiratory Viruses 10*, 375-385.

Emukule, G. O., Otiato, F., Nyawanda, B. O., Otieno, N. A., Ochieng, C. A., Ndegwa, L. K., Muturi, P., Bigogo, G., Verani, J. R., Muthoka, P. M., Hunsperger, E., Chaves, S. S. (2019) 'The Epidemiology and Burden of Influenza B/Victoria and B/Yamagata Lineages in Kenya, 2012-2016'. *Open Forum Infect Dis 6*, ofz421.

Emukule, G. O., Paget, J., van der Velden, K., Mott, J. A. (2015) 'Influenza-Associated Disease Burden in Kenya: A Systematic Review of Literature'. *PLoS One 10*, e0138708.

Faria, N. R., Quick, J., Claro, I. M., Theze, J., de Jesus, J. G., Giovanetti, M., Kraemer, M. U. G., Hill, S. C., Black, A., da Costa, A. C., Franco, L. C., Silva, S. P., Wu, C. H., Raghwani, J., Cauchemez, S., du Plessis, L., Verotti, M. P., de Oliveira, W. K., Carmo, E. H., Coelho, G. E., Santelli, A., Vinhal, L. C., Henriques, C. M., Simpson, J. T., Loose, M., Andersen, K. G., Grubaugh, N. D., Somasekar, S., Chiu, C. Y., Munoz-Medina, J. E., Gonzalez-Bonilla, C. R., Arias, C. F., Lewis-Ximenez, L. L., Baylis, S. A., Chieppe, A. O., Aguiar, S. F., Fernandes, C. A., Lemos, P. S., Nascimento, B. L. S., Monteiro, H. A. O., Siqueira, I. C., de Queiroz, M. G., de Souza, T. R., Bezerra, J. F., Lemos, M. R., Pereira, G. F., Loudal, D., Moura, L. C., Dhalia, R., Franca, R. F., Magalhaes, T., Marques, E. T., Jr., Jaenisch, T., Wallau, G. L., de Lima, M. C., Nascimento, V., de Cerqueira, E. M., de Lima, M. M., Mascarenhas, D. L., Neto, J. P. M., Levin, A. S., Tozetto-Mendoza, T. R., Fonseca, S. N., Mendes-Correa, M. C., Milagres, F. P., Segurado, A., Holmes, E. C., Rambaut, A., Bedford, T., Nunes, M. R. T., Sabino, E. C., Alcantara, L. C. J., Loman, N. J., Pybus, O. G. (2017) 'Establishment and cryptic transmission of Zika virus in Brazil and the Americas'. *Nature 546*, 406-410.

Faria, N. R., Rambaut, A., Suchard, M. A., Baele, G., Bedford, T., Ward, M. J., Tatem, A. J., Sousa, J. D., Arinaminpathy, N., Pépin, J., Posada, D., Peeters, M., Pybus, O. G., Lemey, P. (2014) 'The early spread and epidemic ignition of HIV-1 in human populations'. *Science 346*, 56.

Faria, N. R., Suchard, M. A., Rambaut, A., Lemey, P. (2011) 'Toward a quantitative understanding of viral phylogeography'. *Curr Opin Virol 1*, 423-429.

Fedonin, G. G., Fantin, Y. S., Favorov, A. V., Shipulin, G. A., Neverov, A. D. (2019) 'VirGenA: a reference-based assembler for variable viral genomes'. *Brief Bioinform 20*, 15-25.

Feikin, D. R., Fu, W., Park, D. E., Shi, Q., Higdon, M. M., Baggett, H. C., Brooks, W. A., Deloria Knoll, M., Hammitt, L. L., Howie, S. R. C., Kotloff, K. L., Levine, O. S., Madhi, S. A., Scott, J. A. G., Thea, D. M., Adrian, P. V., Antonio, M., Awori, J. O., Baillie, V. L., DeLuca, A. N., Driscoll, A. J., Ebruke, B. E., Goswami, D., Karron, R. A., Li, M., Morpeth, S. C., Mwaba, J., Mwansa, J., Prosperi, C., Sawatwong, P., Sow, S. O., Tapia, M. D., Whistler, T., Zaman, K., Zeger, S. L., KL, O. B., Murdoch, D. R., Group, P. S. (2017) 'Is Higher Viral Load in the Upper Respiratory Tract Associated With Severe Pneumonia? Findings From the PERCH Study'. *Clin Infect Dis 64*, S337-S346.

Feikin, D. R., Olack, B., Bigogo, G. M., Audi, A., Cosmas, L., Aura, B., Burke, H., Njenga, M. K., Williamson, J., Breiman, R. F. (2011) 'The burden of common infectious disease syndromes at the clinic and household level from population-based surveillance in rural and urban Kenya'. *PLoS One 6*, e16085.

Fielding, J. E., Kelly, H. A., Glass, K. (2015) 'Transmission of the First Influenza A(H1N1)pdm09 Pandemic Wave in Australia Was Driven by Undetected Infections: Pandemic Response Implications'. *PLoS One 10*, e0144331.

Francis, T. (1940) 'A NEW TYPE OF VIRUS FROM EPIDEMIC INFLUENZA'. *Science 92*, 405.

Francis, T., Quilligan, J. J., Minuse, E. (1950) 'Identification of Another Epidemic Respiratory Disease'. *Science 112*, 495.

Francis, T., Salk, J. E., Pearson, H. E., Brown, P. N. (1945) 'PROTECTIVE EFFECT OF VACCINATION AGAINST INDUCED INFLUENZA A'. *J Clin Invest 24*, 536-546.

Fraser, C., Donnelly, C. A., Cauchemez, S., Hanage, W. P., Van Kerkhove, M. D., Hollingsworth, T. D., Griffin, J., Baggaley, R. F., Jenkins, H. E., Lyons, E. J., Jombart, T., Hinsley, W. R., Grassly, N. C., Balloux, F., Ghani, A. C., Ferguson, N. M., Rambaut, A., Pybus, O. G., Lopez-Gatell, H., Alpuche-Aranda, C. M., Chapela, I. B., Zavala, E. P., Guevara, D. M., Checchi, F., Garcia, E., Hugonnet, S., Roth, C., Collaboration, W. H. O. R. P. A. (2009) 'Pandemic potential of a strain of influenza A (H1N1): early findings'. *Science 324*, 1557-1561.

Gachara, G., Symekher, S., Otieno, M., Magana, J., Opot, B., Bulimo, W. (2016) 'Whole genome characterization of human influenza A(H1N1)pdm09 viruses isolated from Kenya during the 2009 pandemic'. *Infection, Genetics and Evolution 40*, 98-103.

Galiano, M., Agapow, P. M., Thompson, C., Platt, S., Underwood, A., Ellis, J., Myers, R., Green, J., Zambon, M. (2011) 'Evolutionary pathways of the pandemic influenza A (H1N1) 2009 in the UK'. *PLoS One 6*, e23779.

Gargis, A. S., Kalman, L., Lubin, I. M. (2016) 'Assuring the Quality of Next-Generation Sequencing in Clinical Microbiology and Public Health Laboratories'. *J Clin Microbiol 54*, 2857-2865.

Garten, R. J., Davis, C. T., Russell, C. A., Shu, B., Lindstrom, S., Balish, A., Sessions, W. M., Xu, X., Skepner, E., Deyde, V., Okomo-Adhiambo, M., Gubareva, L., Barnes, J., Smith, C. B., Emery, S. L., Hillman, M. J., Rivailler, P., Smagala, J., de Graaf, M., Burke, D. F., Fouchier, R. A., Pappas, C., Alpuche-Aranda, C. M., Lopez-Gatell, H., Olivera, H., Lopez, I., Myers, C. A., Faix, D., Blair, P. J., Yu, C., Keene, K. M., Dotson, P. D., Jr., Boxrud, D., Sambol, A. R., Abid, S. H., St George, K., Bannerman, T., Moore, A. L., Stringer, D. J., Blevins, P., Demmler-Harrison, G. J., Ginsberg, M., Kriner, P., Waterman, S., Smole, S., Guevara, H. F., Belongia, E. A., Clark, P. A., Beatrice, S. T., Donis, R., Katz, J., Finelli, L., Bridges, C. B., Shaw, M., Jernigan, D. B., Uyeki, T. M., Smith, D. J., Klimov, A. I., Cox, N. J. (2009) 'Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans'. *Science 325*, 197-201.

Gatherer, D. (2009) 'The 2009 H1N1 influenza outbreak in its historical context'. *J Clin Virol 45*, 174-178.

Geoghegan, J. L., Saavedra, A. F., Duchene, S., Sullivan, S., Barr, I., Holmes, E. C. (2018) 'Continental synchronicity of human influenza virus epidemics despite climatic variation'. *PLoS Pathog 14*, e1006780.

Gessner, B. D., Shindo, N., Briand, S. (2011) 'Seasonal influenza epidemiology in sub-Saharan Africa: a systematic review'. *The Lancet Infectious Diseases 11*, 223-235.

Ghedin, E., Laplante, J., DePasse, J., Wentworth, D. E., Santos, R. P., Lepow, M. L., Porter, J., Stellrecht, K., Lin, X., Operario, D., Griesemer, S., Fitch, A., Halpin, R. A., Stockwell, T. B., Spiro, D. J., Holmes, E. C., St George, K. (2011) 'Deep sequencing reveals mixed infection with 2009 pandemic influenza A (H1N1) virus strains and the emergence of oseltamivir resistance'. *J Infect Dis 203*, 168-174.

Ghedin, E., Sengamalay, N. A., Shumway, M., Zaborsky, J., Feldblyum, T., Subbu, V., Spiro, D. J., Sitz, J., Koo, H., Bolotov, P., Dernovoy, D., Tatusova, T., Bao, Y., St George, K., Taylor, J., Lipman, D. J., Fraser, C. M., Taubenberger, J. K., Salzberg, S. L. (2005) 'Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution'. *Nature 437*, 1162-1166.

Goldstein, E. J., Harvey, W. T., Wilkie, G. S., Shepherd, S. J., MacLean, A. R., Murcia, P. R., Gunson, R. N. (2017) 'Integrating patient and whole-genome sequencing data to provide insights into the epidemiology of seasonal influenza A (H3N2) viruses'. *Microbial Genomics 4*.

Grenfell, B. T., Pybus, O. G., Gog, J. R., Wood, J. L. N., Daly, J. M., Mumford, J. A., Holmes, E. C. (2004) 'Unifying the epidemiological and evolutionary dynamics of pathogens'. *Science 303*, 327+.

Hadfield, J., Megill, C., Bell, S. M., Huddleston, J., Potter, B., Callender, C., Sagulenko, P., Bedford, T., Neher, R. A. (2018) 'Nextstrain: real-time tracking of pathogen evolution'. *Bioinformatics 34*, 4121-4123.

Hammitt, L. L., Kazungu, S., Welch, S., Bett, A., Onyango, C. O., Gunson, R. N., Scott, J. A. G., Nokes, D. J. (2011) 'Added Value of an Oropharyngeal Swab in Detection of Viruses in Children Hospitalized with Lower Respiratory Tract Infection '. *Journal of Clinical Microbiology 49*, 2318–2320.

Han, A. X., Parker, E., Scholer, F., Maurer-Stroh, S., Russell, C. A. (2019) 'Phylogenetic Clustering by Linear Integer Programming (PhyCLIP)'. *Mol Biol Evol 36*, 1580-1595.

Hause, B. M., Collin, E. A., Liu, R., Huang, B., Sheng, Z., Lu, W., Wang, D., Nelson, E. A., Li, F. (2014) 'Characterization of a novel influenza virus in cattle and swine: proposal for a new genus in the Orthomyxoviridae family'. *mBio 5*, e00031-00014.

Hayden, F., Palese, P. (2017) 'Influenza Virus'. In *Richman D, Whitley R, Hayden F (ed), Clinical Virology* (Washington, DC, ASM Press), pp. 1009-1058.

Hedge, J., Lycett, S. J., Rambaut, A. (2013) 'Real-time characterization of the molecular epidemiology of an influenza pandemic'. *Biol Lett 9*, 20130331.

Hirve, S., Newman, L. P., Paget, J., Azziz-Baumgartner, E., Fitzner, J., Bhat, N., Vandemaele, K., Zhang, W. (2016) 'Influenza Seasonality in the Tropics and Subtropics – When to Vaccinate?'. *PLOS ONE 11*, e0153003.

Holmes, E. C. (2008) 'Evolutionary history and phylogeography of human viruses'. *Annu Rev Microbiol 62*, 307-328.

Holmes, E. C., Ghedin, E., Halpin, R. A., Stockwell, T. B., Zhang, X. Q., Fleming, R., Davey, R., Benson, C. A., Mehta, S., Taplitz, R., Liu, Y. T., Brouwer, K. C., Wentworth, D. E., Lin, X., Schooley, R. T., Group, I. F. S. (2011) 'Extensive geographical mixing of 2009 human H1N1 influenza A virus in a single university community'. *J Virol 85*, 6923-6929.

Holmes, E. C., Ghedin, E., Miller, N., Taylor, J., Bao, Y., St George, K., Grenfell, B. T., Salzberg, S. L., Fraser, C. M., Lipman, D. J., Taubenberger, J. K. (2005) 'Whole-genome analysis of human influenza A virus reveals multiple persistent lineages and reassortment among recent H3N2 viruses'. *PLoS Biol 3*, e300.

Hoper, D., Hoffmann, B., Beer, M. (2011) 'A comprehensive deep sequencing strategy for full-length genomes of influenza A'. *PLoS One 6*, e19075.

Houghton, R., Ellis, J., Galiano, M., Clark, T. W., Wyllie, S. (2017) 'Haemagglutinin and neuraminidase sequencing delineate nosocomial influenza outbreaks with accuracy equivalent to whole genome sequencing'. *J Infect 74*, 377-384.

Hunt, M., Gall, A., Ong, S. H., Brener, J., Ferns, B., Goulder, P., Nastouli, E., Keane, J. A., Kellam, P., Otto, T. D. (2015) 'IVA: accurate de novo assembly of RNA virus genomes'. *Bioinformatics 31*, 2374-2376.

Illumina. 2020. 'Sequencing the Rapidly Evolving Influenza A Virus on the MiSeq System' [Online]. Available: https://www.illumina.com/content/dam/illumina-marketing/documents/products/appnotes/miseq-nextera-xt-influenza-application-note-770-2015-053.pdf [Accessed May 2020].

Imai, K., Tamura, K., Tanigaki, T., Takizawa, M., Nakayama, E., Taniguchi, T., Okamoto, M., Nishiyama, Y., Tarumoto, N., Mitsutake, K., Murakami, T., Maesaki, S., Maeda, T. (2018) 'Whole Genome Sequencing of Influenza A and B Viruses With the MinION Sequencer in the Clinical Setting: A Pilot Study'. *Front Microbiol 9*, 2748.

Iqbal, Z., Caccamo, M., Turner, I., Flicek, P., McVean, G. (2012) 'De novo assembly and genotyping of variants using colored de Bruijn graphs'. *Nat Genet 44*, 226-232.

Iuliano, A. D., Roguski, K. M., Chang, H. H., Muscatello, D. J., Palekar, R., Tempia, S., Cohen, C., Gran, J. M., Schanzer, D., Cowling, B. J., Wu, P., Kyncl, J., Ang, L. W., Park, M., Redlberger-Fritz, M., Yu, H., Espenhain, L., Krishnan, A., Emukule, G., van Asten, L., Pereira da Silva, S., Aungkulanon, S., Buchholz, U., Widdowson, M.-A., Bresee, J. S., Azziz-Baumgartner, E., Cheng,

P.-Y., Dawood, F., Foppa, I., Olsen, S., Haber, M., Jeffers, C., MacIntyre, C. R., Newall, A. T., Wood, J. G., Kundi, M., Popow-Kraupp, T., Ahmed, M., Rahman, M., Marinho, F., Sotomayor Proschle, C. V., Vergara Mallegas, N., Luzhao, F., Sa, L., Barbosa-Ramírez, J., Sanchez, D. M., Gomez, L. A., Vargas, X. B., Acosta Herrera, a., Llanés, M. J., Fischer, T. K., Krause, T. G., Mølbak, K., Nielsen, J., Trebbien, R., Bruno, A., Ojeda, J., Ramos, H., an der Heiden, M., del Carmen Castillo Signor, L., Serrano, C. E., Bhardwaj, R., Chadha, M., Narayan, V., Kosen, S., Bromberg, M., Glatman-Freedman, A., Kaufman, Z., Arima, Y., Oishi, K., Chaves, S., Nyawanda, B., Al-Jarallah, R. A., Kuri-Morales, P. A., Matus, C. R., Corona, M. E. J., Burmaa, A., Darmaa, O., Obtel, M., Cherkaoui, I., van den Wijngaard, C. C., van der Hoek, W., Baker, M., Bandaranayake, D., Bissielo, A., Huang, S., Lopez, L., Newbern, C., Flem, E., Grøneng, G. M., Hauge, S., de Cosío, F. G., de Moltó, Y., Castillo, L. M., Cabello, M. A., von Horoch, M., Medina Osis, J., Machado, A., Nunes, B., Rodrigues, A. P., Rodrigues, E., Calomfirescu, C., Lupulescu, E., Popescu, R., Popovici, O., Bogdanovic, D., Kostic, M., Lazarevic, K., Milosevic, Z., Tiodorovic, B., Chen, M., Cutter, J., Lee, V., Lin, R., Ma, S., Cohen, A. L., Treurnicht, F., Kim, W. J., Delgado-Sanz, C., de mateo Ontañón, S., Larrauri, A., León, I. L., Vallejo, F., Born, R., Junker, C., Koch, D., Chuang, J.-H., Huang, W.-T., Kuo, H.-W., Tsai, Y.-C., Bundhamcharoen, K., Chittaganpitch, M., Green, H. K., Pebody, R., Goñi, N., Chiparelli, H., Brammer, L., Mustaquim, D. (2018) 'Estimates of global seasonal influenza-associated respiratory mortality: a modelling study'. *The Lancet 391*, 1285-1300.

Johnson, N. P., Mueller, J. (2002) 'Updating the accounts: global mortality of the 1918-1920 "Spanish" influenza pandemic'. *Bull Hist Med 76*, 105-115.

Kalyaanamoorthy, S., Minh, B. Q., Wong, T. K. F., von Haeseler, A., Jermiin, L. S. (2017) 'ModelFinder: fast model selection for accurate phylogenetic estimates'. *Nat Methods 14*, 587-589.

Katz, M. A., Lebo, E., Emukule, G., Njuguna, H. N., Aura, B., Cosmas, L., Audi, A., Junghae, M., Waiboci, L. W., Olack, B., Bigogo, G., Njenga, M. K., Feikin, D. R., Breiman, R. F. (2012a) 'Epidemiology, Seasonality, and Burden of Influenza and Influenza-Like Illness in Urban and Rural Kenya, 2007-2013;2010'. *The Journal of Infectious Diseases 206*, S53-S60.

Katz, M. A., Muthoka, P., Emukule, G. O., Kalani, R., Njuguna, H., Waiboci, L. W., Ahmed, J. A., Bigogo, G., Feikin, D. R., Njenga, M. K., Breiman, R. F., Mott, J. A. (2014) 'Results From the First Six Years of National Sentinel Surveillance for Influenza in Kenya, July 2007–June 2013'. *PLoS ONE 9*, e98615.

Katz, M. A., Schoub, B. D., Heraud, J. M., Breiman, R. F., Njenga, M. K., Widdowson, M. A. (2012b) 'Influenza in Africa: uncovering the epidemiology of a long-overlooked disease'. *J Infect Dis 206 Suppl 1*, S1-4.

Kilbourne, E. D. (2006) 'Influenza pandemics of the 20th century'. *Emerging infectious diseases 12*, 9-14.

Kim, C., Ahmed, J. A., Eidex, R. B., Nyoka, R., Waiboci, L. W., Erdman, D., Tepo, A., Mahamud, A. S., Kabura, W., Nguhi, M., Muthoka, P., Burton, W., Breiman, R. F., Njenga, M. K., Katz, M. A. (2011) 'Comparison of nasopharyngeal and oropharyngeal swabs for the diagnosis of eight respiratory viruses by real-time reverse transcription-PCR assays'. *PLoS One 6*, e21610.

Kiyuka, P. K., Agoti, C. N., Munywoki, P. K., Njeru, R., Bett, A., Otieno, J. R., Otieno, G. P., Kamau, E., Clark, T. G., van der Hoek, L., Kellam, P., Nokes, D. J., Cotten, M. (2018) 'Human Coronavirus NL63 Molecular Epidemiology and Evolutionary Patterns in Rural Coastal Kenya'. *The Journal of Infectious Diseases 217*, 1728-1739.

Klimov, A. I., Garten, R., Russell, C., Barr, I. G., Besselaar, T. G., Daniels, R., Engelhardt, O. G., Grohmann, G., Itamura, S., Kelso, A., McCauley, J., Odagiri, T., Smith, D., Tashiro, M., Xu, X., Webby, R., Wang, D., Ye, Z., Yuelong, S., Zhang, W., Cox, N., Writing Committee of the World Health Organization Consultation on Southern Hemisphere Influenza Vaccine Composition, f. (2012) 'WHO recommendations for the viruses to be used in the 2012 Southern Hemisphere Influenza Vaccine: epidemiology, antigenic and genetic characteristics of influenza A(H1N1)pdm09, A(H3N2) and B influenza viruses collected from February to September 2011'. *Vaccine 30*, 6461-6471.

KNBS (2010) 'Kenya Demographic and Health Survey 2008–2009' (Kenya National Bureau of Statistics).

Kosakovsky Pond, S. L., Chan, J., Holmes, A., Rabadan, R. (2010) 'Network Analysis of Global Influenza Spread'. *PLoS Comput Biol 6*.

Krammer, F., Smith, G. J. D., Fouchier, R. A. M., Peiris, M., Kedzierska, K., Doherty, P. C., Palese, P., Shaw, M. L., Treanor, J., Webster, R. G., García-Sastre, A. (2018) 'Influenza'. *Nature Reviews Disease Primers 4*, 3.

Lafond, K. E., Nair, H., Rasooly, M. H., Valente, F., Booy, R., Rahman, M., Kitsutani, P., Yu, H., Guzman, G., Coulibaly, D., Armero, J., Jima, D., Howie, S. R., Ampofo, W., Mena, R., Chadha, M., Sampurno, O. D., Emukule, G. O., Nurmatov, Z., Corwin, A., Heraud, J. M., Noyola, D. E., Cojocaru, R., Nymadawa, P., Barakat, A., Adedeji, A., von Horoch, M., Olveda, R., Nyatanyi, T., Venter, M., Mmbaga, V., Chittaganpitch, M., Nguyen, T. H., Theo, A., Whaley, M., Azziz-Baumgartner, E., Bresee, J., Campbell, H., Widdowson, M. A., Global Respiratory Hospitalizations-Influenza Proportion Positive Working, G. (2016) 'Global Role and Burden of Influenza in Pediatric Respiratory Hospitalizations, 1982-2012: A Systematic Analysis'. *PLoS Med 13*, e1001977.

Lakspere, T., Tynell, J., Kaloinen, M., Vanlede, M., Parsons, A., Ikonen, N., Kallio-Kokko, H., Kantele, A., Mattila, P., Almusa, H., Julkunen, I., Kainov, D., Kakkola, L. (2014) 'Full-Genome Sequences of Influenza A(H1N1)pdm09 Viruses Isolated from Finnish Patients from 2009 to 2013'. *Genome Announc 2*.

Langmead, B., Trapnell, C., Pop, M., Salzberg, S. L. (2009) 'Ultrafast and memory-efficient alignment of short DNA sequences to the human genome'. *Genome Biol 10*, R25.

Langmuir, A. D., Worthen, T. D., Solomon, J., Ray, C. G., Petersen, E. (1985) 'The Thucydides Syndrome'. *New England Journal of Medicine 313*, 1027-1030.

Larsson, A. (2014) 'AliView: a fast and lightweight alignment viewer and editor for large datasets'. *Bioinformatics 30*, 3276-3278.

Le, M. Q., Lam, H. M., Cuong, V. D., Lam, T. T.-Y., Halpin, R. A., Wentworth, D. E., Hien, N. T., Thanh, L. T., Phuong, H. V. M., Horby, P., Boni, M. F. (2013) 'Migration and Persistence of Human Influenza A Viruses, Vietnam, 2001–2008'. *Emerging Infectious Diseases 19*, 1756-1765.

Lee, H. K., Lee, C. K., Tang, J. W., Loh, T. P., Koay, E. S. (2016) 'Contamination-controlled high-throughput whole genome sequencing for influenza A viruses using the MiSeq sequencer'. *Sci Rep 6*, 33318.

Leigh, J. W., Bryant, D., Nakagawa, S. (2015) 'popart: full-feature software for haplotype network construction'. *Methods in Ecology and Evolution 6*, 1110-1116.

Lemey, P., Rambaut, A., Bedford, T., Faria, N., Bielejec, F., Baele, G., Russell, C. A., Smith, D. J., Pybus, O. G., Brockmann, D., Suchard, M. A. (2014) 'Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2'. *PLoS Pathog 10*, e1003932.

Lemey, P., Rambaut, A., Drummond, A. J., Suchard, M. A. (2009a) 'Bayesian phylogeography finds its roots'. *PLoS Comput Biol 5*, e1000520-e1000520.

Lemey, P., Rambaut, A., Welch, J. J., Suchard, M. A. (2010) 'Phylogeography takes a relaxed random walk in continuous space and time'. *Mol Biol Evol 27*, 1877-1885.

Lemey, P., Suchard, M., Rambaut, A. (2009b) 'Reconstructing the initial global spread of a human influenza pandemic: a Bayesian spatial-temporal model for the global spread of H1N1pdm'. *PLoS Curr Biol 1*.

Levine, O. S., O'Brien, K. L., Deloria-Knoll, M., Murdoch, D. R., Feikin, D. R., DeLuca, A. N., Driscoll, A. J., Baggett, H. C., Brooks, W. A., Howie, S. R., Kotloff, K. L., Madhi, S. A., Maloney, S. A., Sow, S., Thea, D. M., Scott, J. A. (2012) 'The Pneumonia Etiology Research for Child Health Project: a 21st century childhood pneumonia etiology study'. *Clin Infect Dis 54 Suppl 2*, S93-101.

Li, H., Durbin, R. (2009) 'Fast and accurate short read alignment with Burrows-Wheeler transform'. *Bioinformatics 25*, 1754-1760.

Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N., Marth, G., Abecasis, G., Durbin, R., Genome Project Data Processing, S. (2009) 'The Sequence Alignment/Map format and SAMtools'. *Bioinformatics 25*, 2078-2079.

Li, P. E., Lo, C. C., Anderson, J. J., Davenport, K. W., Bishop-Lilly, K. A., Xu, Y., Ahmed, S., Feng, S., Mokashi, V. P., Chain, P. S. (2017) 'Enabling the democratization of the genomics revolution with a fully integrated web-based bioinformatics platform'. *Nucleic Acids Res 45*, 67-80.

Lycett, S., McLeish, N. J., Robertson, C., Carman, W., Baillie, G., McMenamin, J., Rambaut, A., Simmonds, P., Woolhouse, M., Leigh Brown, A. J. (2012) 'Origin and fate of A/H1N1 influenza in Scotland during 2009'. *J Gen Virol 93*, 1253-1260.

Maljkovic Berry, I., Melendrez, M. C., Bishop-Lilly, K. A., Rutvisuttinunt, W., Pollett, S., Talundzic, E., Morton, L., Jarman, R. G. (2020) 'Next Generation Sequencing and Bioinformatics Methodologies for Infectious Disease Research and Public Health: Approaches, Applications, and Considerations for Development of Laboratory Capacity'. *J Infect Dis 221*, S292-S307.

Meinel, D. M., Heinzinger, S., Eberle, U., Ackermann, N., Schonberger, K., Sing, A. (2018) 'Whole genome sequencing identifies influenza A H3N2 transmission and offers superior resolution to classical typing methods'. *Infection 46*, 69-76.

Murdoch, D. R., O'Brien, K. L., Driscoll, A. J., Karron, R. A., Bhat, N. (2012) 'Laboratory Methods for Determining Pneumonia Etiology in Children'. *Clinical Infectious Diseases 54*, S146-S152.

Nagarajan, N., Kingsford, C. (2011) 'GiRaF: robust, computational identification of influenza reassortments via graph mining'. *Nucleic Acids Research 39*, e34-e34.

Nelson, M., Spiro, D., Wentworth, D., Beck, E., Fan, J., Ghedin, E., Halpin, R., Bera, J., Hine, E., Proudfoot, K., Stockwell, T., Lin, X., Griesemer, S., Kumar, S., Bose, M., Viboud, C., Holmes, E., Henrickson, K. (2009) 'The early diversification of influenza A/H1N1pdm'. *PLoS Curr 1*, RRN1126.

Nelson, M. I., Edelman, L., Spiro, D. J., Boyne, A. R., Bera, J., Halpin, R., Sengamalay, N., Ghedin, E., Miller, M. A., Simonsen, L., Viboud, C., Holmes, E. C. (2008) 'Molecular epidemiology of A/H3N2 and A/H1N1 influenza virus during a single epidemic season in the United States'. *PLoS Pathog 4*, e1000133.

Nelson, M. I., Njouom, R., Viboud, C., Niang, M. N., Kadjo, H., Ampofo, W., Adebayo, A., Tarnagda, Z., Miller, M. A., Holmes, E. C., Diop, O. M. (2014) 'Multiyear persistence of 2 pandemic A/H1N1 influenza virus lineages in West Africa'. *J Infect Dis 210*, 121-125.

Nelson, M. I., Simonsen, L., Viboud, C., Miller, M. A., Holmes, E. C. (2007) 'Phylogenetic Analysis Reveals the Global Migration of Seasonal Influenza A Viruses'. *PLoS Pathogens 3*.

Nelson, M. I., Simonsen, L., Viboud, C., Miller, M. A., Taylor, J., George, K. S., Griesemer, S. B., Ghedin, E., Sengamalay, N. A., Spiro, D. J., Volkov, I., Grenfell, B. T., Lipman, D. J., Taubenberger, J. K., Holmes, E. C. (2006) 'Stochastic processes are key determinants of short-term evolution in influenza a virus'. *PLoS Pathog 2*, e125.

Nelson, M. I., Tan, Y., Ghedin, E., Wentworth, D. E., St George, K., Edelman, L., Beck, E. T., Fan, J., Lam, T. T., Kumar, S., Spiro, D. J., Simonsen, L., Viboud, C., Holmes, E. C., Henrickson, K. J., Musser, J. M. (2011) 'Phylogeography of the spring and fall waves of the H1N1/09 pandemic influenza virus in the United States'. *J Virol 85*, 828-834.

Newman, L. P., Bhat, N., Fleming, J. A., Neuzil, K. M. (2018) 'Global influenza seasonality to inform country-level vaccine programs: An analysis of WHO FluNet influenza surveillance data between 2011 and 2016'. *PLoS One 13*, e0193263.

Ng, S., Gordon, A. (2015) 'Influenza Burden and Transmission in the Tropics'. *Current Epidemiology Reports 2*, 89-100.

Nguyen, L.-T., Schmidt, H. A., Haeseler, A. v., Minh, B. Q. (2014) 'IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies'. *Molecular Biology evolution 32*, 268-274.

Nokes, D. J., Ngama, M., Bett, A., Abwao, J., Munywoki, P., English, M., Scott, J. A., Cane, P. A., Medley, G. F. (2009) 'Incidence and severity of respiratory syncytial virus pneumonia in rural Kenyan children identified through hospital surveillance'. *Clin Infect Dis 49*, 1341-1349.

Nokes, D. J., Okiro, E. A., Ngama, M., Ochola, R., White, L. J., Scott, P. D., English, M., Cane, P. A., Medley, G. F. (2008) 'Respiratory syncytial virus infection and disease in infants and young children observed from birth in Kilifi District, Kenya'. *Clin Infect Dis 46*, 50-57.

Nyasimi, F. M., Owuor, D. C., Ngoi, J. M., Mwihuri, A. G., Otieno, G. P., Otieno, J. R., Githinji, G., Nyiro, J. U., Nokes, D. J., Agoti, C. N. (2020) 'Epidemiological and evolutionary dynamics of influenza B virus in coastal Kenya as revealed by genomic analysis of strains sampled over a single season'. *Virus Evolution*.

Nyiro, J. U., Munywoki, P., Kamau, E., Agoti, C., Gichuki, A., Etyang, T., Otieno, G., Nokes, D. J. (2018) 'Surveillance of respiratory viruses in the outpatient setting in rural coastal Kenya: baseline epidemiological observations [version 1; referees: 2 approved] '. *Wellcome Open Research 3*.

O'Brien, K. L., Baggett, H. C., Brooks, W. A., Feikin, D. R., Hammitt, L. L., Higdon, M. M., Howie, S. R. C., Deloria Knoll, M., Kotloff, K. L., Levine, O. S., Madhi, S. A., Murdoch, D. R., Prosperi, C., Scott, J. A. G., Shi, Q., Thea, D. M., Wu, Z., Zeger, S. L., Adrian, P. V., Akarasewi, P., Anderson, T. P., Antonio, M., Awori, J. O., Baillie, V. L., Bunthi, C., Chipeta, J., Chisti, M. J., Crawley, J., DeLuca, A. N., Driscoll, A. J., Ebruke, B. E., Endtz, H. P., Fancourt, N., Fu, W., Goswami, D., Groome, M. J., Haddix, M., Hossain, L., Jahan, Y., Kagucia, E. W., Kamau, A., Karron, R. A., Kazungu, S., Kourouma, N., Kuwanda, L., Kwenda, G., Li, M., Machuka, E. M., Mackenzie, G., Mahomed, N., Maloney, S. A., McLellan, J. L., Mitchell, J. L., Moore, D. P., Morpeth, S. C., Mudau, A., Mwananyanda, L., Mwansa, J., Silaba Ominde, M., Onwuchekwa, U., Park, D. E., Rhodes, J., Sawatwong, P., Seidenberg, P., Shamsul, A., Simões, E. A. F., Sissoko, S., Wa Somwe, S., Sow, S. O., Sylla, M., Tamboura, B., Tapia, M. D., Thamthitiwat, S., Toure, A., Watson, N. L., Zaman, K., Zaman, S. M. A. (2019) 'Causes of severe pneumonia requiring hospital admission in children without HIV infection from Africa and Asia: the PERCH multi-country case-control study'. *The Lancet 394*, 757-779.

Odhiambo, F. O., Laserson, K. F., Sewe, M., Hamel, M. J., Feikin, D. R., Adazu, K., Ogwang, S., Obor, D., Amek, N., Bayoh, N., Ombok, M., Lindblade, K., Desai, M., ter Kuile, F., Phillips-Howard, P., van Eijk, A. M., Rosen, D., Hightower, A., Ofware, P., Muttai, H., Nahlen, B., DeCock, K., Slutsker, L., Breiman, R. F., Vulule, J. M. (2012) 'Profile: The KEMRI/CDC Health and Demographic Surveillance System--Western Kenya'. *International Journal of Epidemiology 41*, 977-987.

Onyango, C. O., Njeru, R., Kazungu, S., Achilla, R., Bulimo, W., Welch, S. R., Cane, P. A., Gunson, R. N., Hammitt, L. L., Scott, J. A. G., Berkley, J. A., Nokes, D. J. (2012a) 'Influenza Surveillance Among Children With Pneumonia Admitted to a District Hospital in Coastal Kenya, 2007–2010'. *Journal of Infectious Diseases 2012;206(S1):S61–7 206*, S61-S67.

Onyango, C. O., Welch, S. R., Munywoki, P. K., Agoti, C. N., Bett, A., Ngama, M., Myers, R., Cane, P. A., Nokes, D. J. (2012b) 'Molecular epidemiology of human rhinovirus infections in Kilifi, coastal Kenya'. *J Med Virol 84*, 823-831.

Orton, R. J., Gu, Q., Hughes, J., Maabar, M., Modha, S., Vattipally, S. B., Wilkie, G. S., Davison, A. J. (2016) 'Bioinformatics tools for analysing viral genomic data'. *Rev Sci Tech 35*, 271-285.

Osoro, E. M., Munyua, P., Muthoka, P., Gikundi, S., Njenga, M. K., Lifumo, S., Achilla, R., Waiboci, L., Nzioka, C., Omolo, J., Feikin, D. R., Breiman, R. F., Katz, M. A. (2011) 'Hospitalized patients with pandemic (H1N1) 2009, Kenya'. *Emerg Infect Dis 17*, 1744-1746.

Osterholm, M. T., Kelley, N. S., Sommer, A., Belongia, E. A. (2012) 'Efficacy and effectiveness of influenza vaccines: a systematic review and meta-analysis'. *The Lancet Infectious Diseases 12*, 36-44.

Owor, B. E., Masankwa, G. N., Mwango, L. C., Njeru, R. W., Agoti, C. N., Nokes, D. J. (2016) 'Human metapneumovirus epidemiological and evolutionary patterns in Coastal Kenya, 2007-11'. *BMC Infect Dis 16*, 301.

Owuor, D. C., Ngoi, J. M., Otieno, J. R., Otieno, G. P., Nyasimi, F. M., Nyiro, J. U., Agoti, C. N., Chaves, S. S., Nokes, D. J. (2020) 'Genetic characterization of influenza A(H3N2) viruses circulating in coastal Kenya, 2009-2017'. *Influenza and Other Respiratory Viruses 14*, 320-330.

Oxford Business Group. 2017. 'The Report: Kenya 2017' [Online]. Available: https://www.oxfordbusinessgroup.com/kenya-2017/tourism [Accessed].

Paget, J., Spreeuwenberg, P., Charu, V., Taylor, R. J., Iuliano, A. D., Bresee, J., Simonsen, L., Viboud, C., Global Seasonal Influenza-associated Mortality Collaborator, N., Teams*, G. L. C. (2019) 'Global mortality associated with seasonal influenza epidemics: New burden estimates and predictors from the GLaMOR Project'. *J Glob Health 9*, 020421.

Parker, J., Rambaut, A., Pybus, O. G. (2008) 'Correlating viral phenotypes with phylogeny: Accounting for phylogenetic uncertainty'. *Infection, Genetics and Evolution 8*, 239-246.

Parodi, V., de Florentiis, D., Martini, M., Ansaldi, F. (2011) 'Inactivated Influenza Vaccines'. *Drugs & Aging 28*, 93-106.

Petrova, V. N., Russell, C. A. (2018) 'The evolution of seasonal influenza viruses'. *Nature Reviews Microbiology 16*, 47-60.

Pollett, S., Nelson, M. I., Kasper, M., Tinoco, Y., Simons, M., Romero, C., Silva, M., Lin, X., Halpin, R. A., Fedorova, N., Stockwell, T. B., Wentworth, D., Holmes, E. C., Bausch, D. G. (2015)

'Phylogeography of Influenza A(H3N2) Virus in Peru, 2010-2012'. *Emerg Infect Dis 21*, 1330-1338.

Pybus, O. G. (2016) ' Taming The Beast: Introduction to infectious disease phylodynamics'. *4*.

Pybus, O. G., Rambaut, A. (2009) 'Evolutionary analysis of the dynamics of viral infectious disease'. *Nat Rev Genet 10*, 540-550.

Pybus, O. G., Tatem, A. J., Lemey, P. (2015) 'Virus evolution and transmission in an ever more connected world'. *Proc Biol Sci 282*, 20142878.

Radford, A. D., Chapman, D., Dixon, L., Chantrey, J., Darby, A. C., Hall, N. (2012) 'Application of next-generation sequencing technologies in virology'. *J Gen Virol 93*, 1853-1868.

Rambaut, A., Holmes, E. (2009) 'The early molecular epidemiology of the swine-origin A/H1N1 human influenza pandemic'. *PLoS Currents 1*, RRN1003.

Rambaut, A., Pybus, O. G., Nelson, M. I., Viboud, C., Taubenberger, J. K., Holmes, E. C. (2008) 'The genomic and epidemiological dynamics of human influenza A virus'. *Nature 453*, 615+.

Reimering, S., Munoz, S., McHardy, A. C. (2020) 'Phylogeographic reconstruction using air transportation data and its application to the 2009 H1N1 influenza A pandemic'. *PLoS Comput Biol 16*, e1007101.

Russell, C. A., Jones, T. C., Barr, I. G., Cox, N. J., Garten, R. J., Gregory, V., Gust, I. D., Hampson, A. W., Hay, A. J., Hurt, A. C., de Jong, J. C., Kelso, A., Klimov, A. I., Kageyama, T., Komadina, N., Lapedes, A. S., Lin, Y. P., Mosterin, A., Obuchi, M., Odagiri, T., Osterhaus, A. D. M. E., Rimmelzwaan, G. F., Shaw, M. W., Skepner, E., Stohr, K., Tashiro, M., Fouchier, R. A. M., Smith, D. J. (2008) 'The global circulation of seasonal influenza A (H3N2) viruses'. *Science (New York, NY) 320*, 340-346.

Rutvisuttinunt, W., Chinnawirotpisan, P., Simasathien, S., Shrestha, S. K., Yoon, I. K., Klungthong, C., Fernandez, S. (2013) 'Simultaneous and complete genome sequencing of influenza A and B with high coverage by Illumina MiSeq Platform'. *J Virol Methods 193*, 394-404.

Sagulenko, P., Puller, V., Neher, R. A. (2018) 'TreeTime: Maximum-likelihood phylodynamic analysis'. *Virus Evol 4*, vex042.

Salk, J. E., Suriano, P. C. (1949) 'Importance of antigenic composition of influenza virus vaccine in protecting against the natural disease; observations during the winter of 1947-1948'. *Am J Public Health Nations Health 39*, 345-355.

Sande, C. J., Mutunga, M. N., Medley, G. F., Cane, P. A., Nokes, D. J. (2013) 'Group- and genotype-specific neutralizing antibody responses against respiratory syncytial virus in infants and young children with severe pneumonia'. *J Infect Dis 207*, 489-492.

Scott, J. A., Bauni, E., Moisi, J. C., Ojal, J., Gatakaa, H., Nyundo, C., Molyneux, C. S., Kombe, F., Tsofa, B., Marsh, K., Peshu, N., Williams, T. N. (2012a) 'Profile: The Kilifi Health and Demographic Surveillance System (KHDSS)'. *Int J Epidemiol 41*, 650-657.

Scott, J. A., Wonodi, C., Moisi, J. C., Deloria-Knoll, M., DeLuca, A. N., Karron, R. A., Bhat, N., Murdoch, D. R., Crawley, J., Levine, O. S., O'Brien, K. L., Feikin, D. R., Pneumonia Methods Working, G. (2012b) 'The definition of pneumonia, the assessment of severity, and clinical standardization in the Pneumonia Etiology Research for Child Health study'. *Clin Infect Dis 54 Suppl 2*, S109-116.

Scott, P. D., Ochola, R., Ngama, M., Okiro, E. A., Nokes, D. J., Medley, G. F., Cane, P. A. (2004) 'Molecular epidemiology of respiratory syncytial virus in Kilifi district, Kenya'. *J Med Virol 74*, 344-354.

Selwyn, B. J., Researchers, o. B. o. t. C. D. G. o. B. (1990) 'The Epidemiology of Acute Respiratory Tract Infection in Young Children: Comparison of Findings from Several Developing Countries'. *Reviews of Infectious Diseases 12*, S870-S888.

Seong, M. W., Cho, S. I., Park, H., Seo, S. H., Lee, S. J., Kim, E. C., Park, S. S. (2016) 'Genotyping Influenza Virus by Next-Generation Deep Sequencing in Clinical Specimens'. *Ann Lab Med 36*, 255-258.

Shaw, M., Palese, P. (2013) 'Orthomyxoviridae: the viruses and their replication'. In *Knipe DM, Howley PM (eds), Fields Virology* (Philadelphia, PA, Wolters Kluwer/Lippincott Williams & Wilkins Health), pp. 1151-1185.

Shepard, S. S., Davis, C. T., Bahl, J., Rivailler, P., York, I. A., Donis, R. O. (2014) 'LABEL: fast and accurate lineage assignment with assessment of H5N1 and H9N2 influenza A hemagglutinins'. *PLoS One 9*, e86921.

Shepard, S. S., Meno, S., Bahl, J., Wilson, M. M., Barnes, J., Neuhaus, E. (2016) 'Viral deep sequencing needs an adaptive approach: IRMA, the iterative refinement meta-assembler'. *BMC Genomics 17*, 708.

Simonsen, L., Spreeuwenberg, P., Lustig, R., Taylor, R. J., Fleming, D. M., Kroneman, M., Van Kerkhove, M. D., Mounts, A. W., Paget, W. J., Teams, G. L. C. (2013) 'Global mortality estimates for the 2009 Influenza Pandemic from the GLaMOR project: a modeling study'. *PLoS Med 10*, e1001558.

Smith, D. J., Lapedes, A. S., de Jong, J. C., Bestebroer, T. M., Rimmelzwaan, G. F., Osterhaus, A. D. M. E., Fouchier, R. A. M. (2004) 'Mapping the Antigenic and Genetic Evolution of Influenza Virus'. *Science 305*, 371.

Smith, G. J., Vijaykrishna, D., Bahl, J., Lycett, S. J., Worobey, M., Pybus, O. G., Ma, S. K., Cheung, C. L., Raghwani, J., Bhatt, S., Peiris, J. S., Guan, Y., Rambaut, A. (2009) 'Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic'. *Nature 459*, 1122-1125.

Smith, W., Andrewes, C. H., Laidlaw, P. P. (1933) 'A VIRUS OBTAINED FROM INFLUENZA PATIENTS'. *The Lancet 222*, 66-68.

Sobel Leonard, A., McClain, M. T., Smith, G. J., Wentworth, D. E., Halpin, R. A., Lin, X., Ransier, A., Stockwell, T. B., Das, S. R., Gilbert, A. S., Lambkin-Williams, R., Ginsburg, G. S., Woods, C. W., Koelle, K. (2016) 'Deep Sequencing of Influenza A Virus from a Human Challenge Study Reveals a Selective Bottleneck and Only Limited Intrahost Genetic Diversification'. *J Virol 90*, 11247-11258.

Stöhr, K. (2002) 'Influenza - WHO cares'. *The Lancet Infectious Diseases 2*, 517.

Su, Y. C., Bahl, J., Joseph, U., Butt, K. M., Peck, H. A., Koay, E. S., Oon, L. L., Barr, I. G., Vijaykrishna, D., Smith, G. J. (2015) 'Phylodynamics of H1N1/2009 influenza reveals the transition from host adaptation to immune-driven selection'. *Nat Commun 6*, 7952.

Suchard, M. A., Lemey, P., Baele, G., Ayres, D. L., Drummond, A. J., Rambaut, A. (2018) 'Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10'. *Virus Evolution 4*.

Tang, J. W., Ngai, K. L., Lam, W. Y., Chan, P. K. (2008) 'Seasonality of influenza A(H3N2) virus: a Hong Kong perspective (1997-2006)'. *PLoS One 3*, e2768.

Taubenberger, J. K., Morens, D. M. (2010) 'Influenza: The Once and Future Pandemic'. *Public Health Rep 125 Suppl 3*, 16-26.

Taubenberger, J. K., Reid, A. H., Lourens, R. M., Wang, R., Jin, G., Fanning, T. G. (2005) 'Characterization of the 1918 influenza virus polymerase genes'. *Nature 437*, 889-893.

The PERCH Study Group. 2012. 'The Pneumonia Etiology Research for Child Health Project (PERCH) study materials' [Online]. Available: https://www.jhsph.edu/ivac/resources/perch-background-and-methods/ [Accessed 22 May 2020].

Thorburn, F., Bennett, S., Modha, S., Murdoch, D., Gunson, R., Murcia, P. R. (2015) 'The use of next generation sequencing in the diagnosis and typing of respiratory infections'. *J Clin Virol 69*, 96-100.

Toft, C., Andersson, S. G. E. (2010) 'Evolutionary microbial genomics: insights into bacterial host adaptation'. *Nature Reviews Genetics 11*, 465+.

Tong, S., Zhu, X., Li, Y., Shi, M., Zhang, J., Bourgeois, M., Yang, H., Chen, X., Recuenco, S., Gomez, J., Chen, L.-M., Johnson, A., Tao, Y., Dreyfus, C., Yu, W., McBride, R., Carney, P. J., Gilbert, A. T., Chang, J., Guo, Z., Davis, C. T., Paulson, J. C., Stevens, J., Rupprecht, C. E., Holmes, E. C., Wilson, I. A., Donis, R. O. (2013) 'New World Bats Harbor Diverse Influenza A Viruses'. *PLoS Pathogens 9*, e1003657.

Tong, Y. G., Shi, W. F., Liu, D., Qian, J., Liang, L., Bo, X. C., Liu, J., Ren, H. G., Fan, H., Ni, M., Sun, Y., Jin, Y., Teng, Y., Li, Z., Kargbo, D., Dafae, F., Kanu, A., Chen, C. C., Lan, Z. H., Jiang, H., Luo, Y., Lu, H. J., Zhang, X. G., Yang, F., Hu, Y., Cao, Y. X., Deng, Y. Q., Su, H. X., Sun, Y., Liu, W. S., Wang, Z., Wang, C. Y., Bu, Z. Y., Guo, Z. D., Zhang, L. B., Nie, W. M., Bai, C.

Q., Sun, C. H., An, X. P., Xu, P. S., Zhang, X. L., Huang, Y., Mi, Z. Q., Yu, D., Yao, H. W., Feng, Y., Xia, Z. P., Zheng, X. X., Yang, S. T., Lu, B., Jiang, J. F., Kargbo, B., He, F. C., Gao, G. F., Cao, W. C., China Mobile Laboratory Testing Team in Sierra, L. (2015) 'Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone'. *Nature 524*, 93-96.

Tricco, A. C., Chit, A., Soobiah, C., Hallett, D., Meier, G., Chen, M. H., Tashkandi, M., Bauch, C. T., Loeb, M. (2013) 'Comparing influenza vaccine efficacy against mismatched and matched strains: a systematic review and meta-analysis'. *BMC Med 11*, 153-153.

Tumpey, T. M., Basler, C. F., Aguilar, P. V., Zeng, H., Solórzano, A., Swayne, D. E., Cox, N. J., Katz, J. M., Taubenberger, J. K., Palese, P., García-Sastre, A. (2005) 'Characterization of the Reconstructed 1918 Spanish Influenza Pandemic Virus'. *Science 310*, 77.

United Nations, D. o. E. a. S. A. 2019. 'World Population Prospects 2019: Highlights' [Online]. United Nations. Available: https://population.un.org/wpp/Publications/Files/WPP2019_Highlights.pdf [Accessed 29 June 2020].

Vaidya, G., Lohman, D. J., Meier, R. (2011) 'SequenceMatrix: concatenation software for the fast assembly of multi-gene datasets with character set and codon information'. *Cladistics 27*, 171-180.

Van den Hoecke, S., Verhelst, J., Vuylsteke, M., Saelens, X. (2015) 'Analysis of the genetic diversity of influenza A viruses using next-generation DNA sequencing'. *BMC Genomics 16*, 79.

Van Kerkhove, M. D., Mounts, A. W. (2011) '2009 versus 2010 comparison of influenza activity in southern hemisphere temperate countries'. *Influenza Other Respir Viruses 5*, 375-379.

Venter, M., Naidoo, D., Pretorius, M., Buys, A., McAnerney, J., Blumberg, L., Madhi, S. A., Cohen, C., Schoub, B. (2012) 'Evolutionary dynamics of 2009 pandemic influenza A virus subtype H1N1 in South Africa during 2009-2010'. *J Infect Dis 206 Suppl 1*, S166-172.

Viboud, C., Nelson, M. I., Tan, Y., Holmes, E. C. (2013) 'Contrasting the epidemiological and evolutionary dynamics of influenza spatial transmission'. *Philos Trans R Soc Lond B Biol Sci 368*, 20120199.

Vijaykrishna, D., Holmes, E. C., Joseph, U., Fourment, M., Su, Y. C., Halpin, R., Lee, R. T., Deng, Y. M., Gunalan, V., Lin, X., Stockwell, T. B., Fedorova, N. B., Zhou, B., Spirason, N., Kuhnert, D., Boskova, V., Stadler, T., Costa, A. M., Dwyer, D. E., Huang, Q. S., Jennings, L. C., Rawlinson, W., Sullivan, S. G., Hurt, A. C., Maurer-Stroh, S., Wentworth, D. E., Smith, G. J., Barr, I. G. (2015) 'The contrasting phylodynamics of human influenza B viruses'. *Elife 4*, e05055.

Wang, J., Moore, N. E., Deng, Y. M., Eccles, D. A., Hall, R. J. (2015) 'MinION nanopore sequencing of an influenza genome'. *Front Microbiol 6*, 766.

Wang, X., Li, Y., O'Brien, K. L., Madhi, S. A., Widdowson, M.-A., Byass, P., Omer, S. B., Abbas, Q., Ali, A., Amu, A., Azziz-Baumgartner, E., Bassat, Q., Abdullah Brooks, W., Chaves, S. S., Chung, A., Cohen, C., Echavarria, M., Fasce, R. A., Gentile, A., Gordon, A., Groome, M., Heikkinen, T., Hirve, S., Jara, J. H., Katz, M. A., Khuri-Bulos, N., Krishnan, A., de Leon, O.,

Lucero, M. G., McCracken, J. P., Mira-Iglesias, A., Moïsi, J. C., Munywoki, P. K., Ourohiré, M., Polack, F. P., Rahi, M., Rasmussen, Z. A., Rath, B. A., Saha, S. K., Simões, E. A. F., Sotomayor, V., Thamthitiwat, S., Treurnicht, F. K., Wamukoya, M., Yoshida, L.-M., Zar, H. J., Campbell, H., Nair, H. (2020) 'Global burden of respiratory infections associated with seasonal influenza in children under 5 years in 2018: a systematic review and modelling study'. *The Lancet Global Health 8*, e497-e510.

Watson, S. J., Welkers, M. R., Depledge, D. P., Coulter, E., Breuer, J. M., de Jong, M. D., Kellam, P. (2013) 'Viral population analysis and minority-variant detection using short read next-generation sequencing'. *Philos Trans R Soc Lond B Biol Sci 368*, 20120205.

Webster, R. G., Bean, W. J., Gorman, O. T., Chambers, T. M., Kawaoka, Y. (1992) 'Evolution and ecology of influenza A viruses'. *Microbiol Rev 56*, 152-179.

Westgeest, K. B., de Graaf, M., Fourment, M., Bestebroer, T. M., van Beek, R., Spronken, M. I., de Jong, J. C., Rimmelzwaan, G. F., Russell, C. A., Osterhaus, A. D., Smith, G. J., Smith, D. J., Fouchier, R. A. (2012) 'Genetic evolution of the neuraminidase of influenza A (H3N2) viruses from 1968 to 2009 and its correspondence to haemagglutinin evolution'. *J Gen Virol 93*, 1996-2007.

Westgeest, K. B., Russell, C. A., Lin, X., Spronken, M. I. J., Bestebroer, T. M., Bahl, J., Beek, R. v., Skepner, E., Halpin, R. A., Jong, J. C. d., Rimmelzwaan, G. F., Osterhaus, A. D. M. E., Smith, D. J., Wentworth, D. E., Fouchier, R. A. M., Graaf, M. d. (2014) 'Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011'. *Journal of Virology 88*, 2844-2857.

Wille, M., Holmes, E. C. (2020) 'The Ecology and Evolution of Influenza Viruses'. *Cold Spring Harb Perspect Med 10*.

Wilm, A., Aw, P. P., Bertrand, D., Yeo, G. H., Ong, S. H., Wong, C. H., Khor, C. C., Petric, R., Hibberd, M. L., Nagarajan, N. (2012) 'LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets'. *Nucleic Acids Res 40*, 11189-11201.

World Health Organization (2005) 'Hospital Care for Children: guidelines for the management of common illnesses with limited resources' (World Health Organization).

World Health Organization. 2006. 'Collecting, preserving and shipping specimens for the diagnosis of avian influenza A(H5N1) virus infection. Guide for field operations.' [Online]. Available: https://www.who.int/csr/resources/publications/surveillance/WHO_CDS_EPR_ARO_2006_1/en/ [Accessed].

World Health Organization. 2009. 'WHO recommendation on pandemic (H1N1) 2009 vaccines. Pandemic(H1N1) briefing note 2.' [Online]. Available: https://www.who.int/csr/disease/swineflu/notes/h1n1_vaccine_20090713/en/ [Accessed].

World Health Organization (2010) 'Writing Committee of the WHO Consultation on Clinical Aspects of Pandemic (H1N1) 2009 Influenza. Clinical Aspects of Pandemic 2009 Influenza A (H1N1) Virus Infection'. *New England Journal of Medicine 362*, 1708-1719.

World Health Organization. 2013. 'Pocket book of hospital care for children: guidelines for the management of common childhood illnesses' [Online]. Geneva, Switzerland. [Accessed 2013].

World Health Organization. 2015. 'Recommended composition of influenza virus vaccines for use in the 2015-2016 northern hemisphere influenza season' [Online]. Available: https://www.who.int/influenza/vaccines/virus/recommendations/2015_16_north/en/ [Accessed].

World Health Organization. 2017. 'Influenza: Global Influenza Surveillance and Response System (GISRS)' [Online]. [Accessed 10th May 2018 2018].

World Health Organization. 2018a. 'Influenza (Seasonal) Fact sheet' [Online]. Available: http://www.who.int/mediacentre/factsheets/fs211/en/ [Accessed 1 February 2018].

World Health Organization. 2018b. 'Recommended composition of influenza virus vaccines for use in the 2018-2019 northern hemisphere influenza season' [Online]. Available: https://www.who.int/influenza/vaccines/virus/recommendations/2018_19_north/en/ [Accessed].

World Health Organization. 2019a. 'Next-generation sequencing of influenza viruses: General information for national influenza centres' [Online]. Available: https://www.who.int/influenza/gisrs_laboratory/national_influenza_centres/NGS_guidance_for_NICs.pdf?ua=1 [Accessed 20 May 2020].

World Health Organization. 2019b. 'Recommended composition of influenza virus vaccines for use in the 2019-2020 northern hemisphere influenza season' [Online]. Available: https://www.who.int/influenza/vaccines/virus/recommendations/2019_20_north/en/ [Accessed].

World Health Organization. 2020a. 'Global Influenza Surveillance and Response System (GISRS)' [Online]. Available: https://www.who.int/influenza/gisrs_laboratory/en/ [Accessed 25 June 2020].

World Health Organization. 2020b. 'Recommended composition of influenza virus vaccines for use in the 2020 - 2021 northern hemisphere influenza season' [Online]. Available: https://www.who.int/influenza/vaccines/virus/recommendations/2020-21_north/en/ [Accessed].

World Health Organization. 2021. 'Global Influenza Programme' [Online]. Available: https://www.who.int/teams/global-influenza-programme/vaccines [Accessed January 2021].

Wright, C. F., Morelli, M. J., Thebaud, G., Knowles, N. J., Herzyk, P., Paton, D. J., Haydon, D. T., King, D. P. (2011) 'Beyond the consensus: dissecting within-host viral population diversity of foot-and-mouth disease virus by using next-generation genome sequencing'. *J Virol 85*, 2266-2275.

Wuthrich, D., Lang, D., Muller, N. F., Neher, R. A., Stadler, T., Egli, A. (2019) 'Evaluation of two workflows for whole genome sequencing-based typing of influenza A viruses'. *J Virol Methods 266*, 30-33.

Xue, K. S., Stevens-Ayers, T., Campbell, A. P., Englund, J. A., Pergam, S. A., Boeckh, M., Bloom, J. D. (2017) 'Parallel evolution of influenza across multiple spatiotemporal scales'. *Elife 6*.

Yang, W., Cummings, M. J., Bakamutumaho, B., Kayiwa, J., Owor, N., Namagambo, B., Byaruhanga, T., Lutwama, J. J., O'Donnell, M. R., Shaman, J. (2018) 'Dynamics of influenza in tropical Africa: Temperature, humidity, and co-circulating (sub)types'. *Influenza Other Respir Viruses 12*, 446-456.

Yang, X., Charlebois, P., Gnerre, S., Coole, M. G., Lennon, N. J., Levin, J. Z., Qu, J., Ryan, E. M., Zody, M. C., Henn, M. R. (2012) 'De novo assembly of highly diverse viral populations'. *BMC Genomics 13*, 475.

Yu, G., Smith, D. K., Zhu, H., Guan, Y., Lam, T. T.-Y. (2017) 'ggtree: an r package for visualization and annotation of phylogenetic trees with their covariates and other associated data'. *Methods in Ecology and Evolution 8*, 28-36.

Zehender, G., Pariani, E., Piralla, A., Lai, A., Gabanelli, E., Ranghiero, A., Ebranati, E., Amendola, A., Campanini, G., Rovida, F., Ciccozzi, M., Galli, M., Baldanti, F., Zanetti, A. R. (2012) 'Reconstruction of the evolutionary dynamics of the A(H1N1)pdm09 influenza virus in Italy during the pandemic and post-pandemic phases'. *PLoS One 7*, e47517.

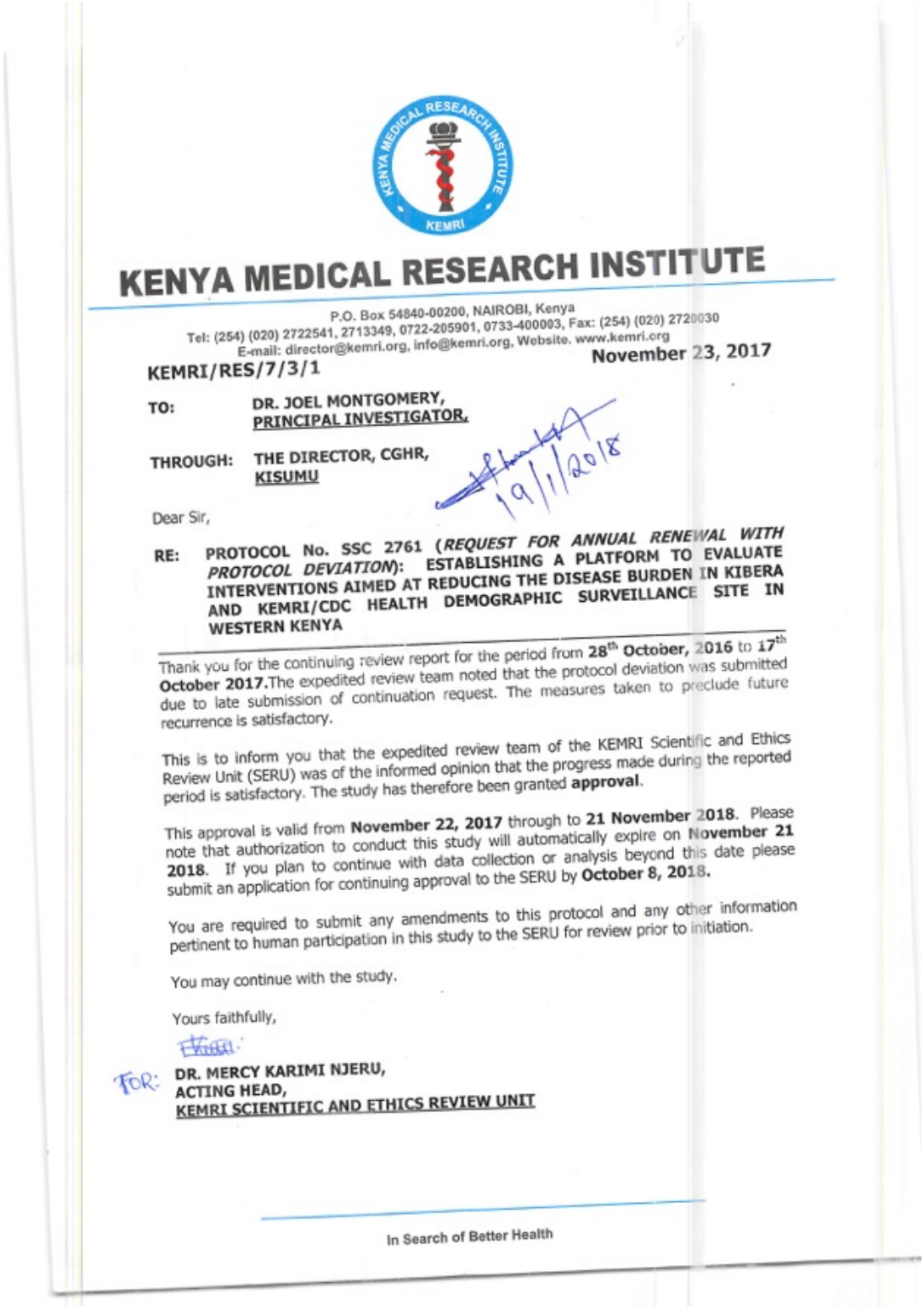
Zhao, M., Lee, W. P., Garrison, E. P., Marth, G. T. (2013) 'SSW library: an SIMD Smith-Waterman C/C++ library for use in genomic applications'. *PLoS One 8*, e82138.

Zhou, B., Donnelly, M. E., Scholes, D. T., St George, K., Hatta, M., Kawaoka, Y., Wentworth, D. E. (2009) 'Single-reaction genomic amplification accelerates sequencing and vaccine production for classical and Swine origin human influenza a viruses'. *J Virol 83*, 10309-10313.

Zhou, B., Wentworth, D. E. (2012) 'Influenza A virus molecular virology techniques'. *Methods Mol Biol 865*, 175-192.

APPENDICES

7.1 Study Scientific and Ethical Approvals



KENYA MEDICAL RESEARCH INSTITUTE

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KEMRI/RES/7/3/1

November 23, 2017

TO: DR. JOEL MONTGOMERY,
PRINCIPAL INVESTIGATOR.

THROUGH: THE DIRECTOR, CGHR,
KISUMU

19/1/2018

Dear Sir,

RE: PROTOCOL No. SSC 2761 (*REQUEST FOR ANNUAL RENEWAL WITH PROTOCOL DEVIATION*): ESTABLISHING A PLATFORM TO EVALUATE INTERVENTIONS AIMED AT REDUCING THE DISEASE BURDEN IN KIBERA AND KEMRI/CDC HEALTH DEMOGRAPHIC SURVEILLANCE SITE IN WESTERN KENYA

Thank you for the continuing review report for the period from **28th October, 2016** to **17th October 2017.**The expedited review team noted that the protocol deviation was submitted due to late submission of continuation request. The measures taken to preclude future recurrence is satisfactory.

This is to inform you that the expedited review team of the KEMRI Scientific and Ethics Review Unit (SERU) was of the informed opinion that the progress made during the reported period is satisfactory. The study has therefore been granted **approval**.

This approval is valid from **November 22, 2017** through to **21 November 2018**. Please note that authorization to conduct this study will automatically expire on **November 21 2018**. If you plan to continue with data collection or analysis beyond this date please submit an application for continuing approval to the SERU by **October 8, 2018.**

You are required to submit any amendments to this protocol and any other information pertinent to human participation in this study to the SERU for review prior to initiation.

You may continue with the study.

Yours faithfully,

FOR: DR. MERCY KARIMI NJERU,
ACTING HEAD,
KEMRI SCIENTIFIC AND ETHICS REVIEW UNIT

In Search of Better Health

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KEMRI/RES/7/3/1 **September 13, 2016**

TO: **HENRY NJUGUNA**
PRINCIPAL INVESTIGATOR

THROUGH: **DR. STEPHEN MUNGA**
THE DIRECTOR, CGHR
KISUMU

Dear Sir,

RE: **SSC 2558 (*REQUEST FOR ANNUAL RENEWAL)* INTEGRATED SURVEILLANCE FOR RESPIRATORY PATHOGENS AND HIV AT SIAYA DISTRICT HOSPITAL (SDH), KAREMO DIVISION, NYANZA REGION, KENYA**

Thank you for the continuing review report for the period **21 August, 2015** to **1 August, 2016.**

This is to inform that during the 255th Committee A meeting of the KEMRI Scientific and Ethics Review Unit (SERU) held on 13 September, 2016, the Committee **conducted the annual review and approved** the above referenced application for another year.

This approval is valid from **13 September, 2016** through to **12 September, 2017**. Please note that authorization to conduct this study will automatically expire on **12th September, 2017**. If you plan to continue with data collection or analysis beyond this date please submit an application for continuing approval to the **SERU** by **31 July, 2017.**

You are required to submit any amendments to this protocol and other information pertinent to human participation in this study to the SERU for review prior to initiation.

Yours faithfully,

FOR: **DR. EVANS AMUKOYE,**
ACTING HEAD
KEMRI/SCIENTIFIC AND ETHICS REVIEW UNIT

JOHNS HOPKINS
BLOOMBERG SCHOOL
of PUBLIC HEALTH

PERCH
Pneumonia Etiology Research for Child Health

Department of International Health

November 17, 2016

Dear Scientific and Ethical Review Committee,

This letter is to inform you that the Executive Committee of the Pneumonia Etiology Research for Child Health (PERCH) study has approved the following PERCH sub-study to be carried out at KEMRI/Wellcome Trust under the leadership of Dr. James Nokes:

Studying the Pathways of Respiratory Virus Disease transmission in Africa (SPReD-Africa)

The objectives of the study are to a) characterize the molecular epidemiology and evolutionary phylogenetics of respiratory viral pathogens detected at the 5 PERCH African sites (The Gambia, Mali, Kenya, Zambia, and South Africa), b) identify the source of viruses introduced to each of the African sites using WGS data for specific respiratory viruses, and c) characterize the genetic phylogeography and genetic relatedness of key respiratory viruses at the PERCH African study sites.

The PERCH Executive Committee, consisting of the study-wide principal investigator at Johns Hopkins Bloomberg School of Public Health, Dr. Kate O'Brien, the 7 PERCH site principal investigators, the study clinical lead, and the study laboratory lead agreed to proceed with shipping and testing of nasopharyngeal/oropharyngeal case and control specimens positive for key respiratory viruses to KEMRI/Wellcome Trust for testing as outlined in the protocol of this study. In addition to sharing specimens, relevant de-identified PERCH data will be shared with the sub-study investigators to aid in interpretation of results. A Material Transfer Agreement and Confidential Disclosure Agreement will be executed prior to shipping specimens and sharing data.

We look forward to collaborating with KEMRI/Wellcome trust on this sub-study which has important public health implications.

Sincerely,

Katherine O'Brien
Professor, International Health
Executive Director, International Vaccine Access Center
Principal Investigator, Pneumonia Etiology Research for Child Health (PERCH) Study
Johns Hopkins Bloomberg School of Public Health

7.2 Genome Details for Kenyan and African Genomes from this Study

7.2.1 Influenza A(H1N1)pdm09 Virus, Kenya, 2009-2018

Sample Name	GISAID Accession	Site	Clade	No. of Reads	IAV Reads	PCR Ct	Collection Date
A/Kenya/Kilifi/003/2009_08-Oct-2009	EPI_ISL_426138	Kilifi	6	423,881	2,451	28.05	08-Oct-09
A/Kenya/Kilifi/006/2009_28-Nov-2009	EPI_ISL_426139	Kilifi	7	438,231	107,871	19.32	28-Nov-09
A/Kenya/Kilifi/008/2009_13-Dec-2009	EPI_ISL_426140	Kilifi	7	279,770	208,817	25.88	13-Dec-09
A/Kenya/Kilifi/009/2009_19-Dec-2009	EPI_ISL_426141	Kilifi	7	428,592	199,634	24.54	19-Dec-09
A/Kenya/Kilifi/011/2010_27-Nov-2010	EPI_ISL_426142	Kilifi	6	371,413	246,220	11	27-Nov-10
A/Kenya/Kilifi/012/2010_28-Nov-2010	EPI_ISL_426143	Kilifi	6	488,230	168,169	26.03	28-Nov-10
A/Kenya/Kilifi/013/2010_13-Dec-2010	EPI_ISL_426144	Kilifi	6	409,491	241,507	22.43	13-Dec-10
A/Kenya/Kilifi/014/2010_28-Dec-2010	EPI_ISL_426145	Kilifi	6	409,979	384,582	24.59	28-Dec-10
A/Kenya/Kilifi/016/2011_07-Jan-2011	EPI_ISL_426146	Kilifi	6	395,668	154,687	27.13	07-Jan-11
A/Kenya/Kilifi/018/2011_27-Jan-2011	EPI_ISL_426147	Kilifi	6	293,831	54,740	28.38	27-Jan-11
A/Kenya/Kilifi/020/2011_10-Feb-2011	EPI_ISL_426148	Kilifi	6	500,005	434,901	25.89	10-Feb-11
A/Kenya/Kilifi/021/2011_27-Feb-2011	EPI_ISL_426149	Kilifi	6	555,193	431,908	14.92	27-Feb-11
A/Kenya/Kilifi/022/2011_22-May-2011	EPI_ISL_426150	Kilifi	6	491,438	468,136	18.13	22-May-11
A/Kenya/Kilifi/023/2011_29-Jun-2011	EPI_ISL_426151	Kilifi	6	464,710	445,000	20.68	29-Jun-11
A/Kenya/Kilifi/029/2011_27-Nov-2011	EPI_ISL_426152	Kilifi	6	449,861	228,672	26.75	27-Nov-11
A/Kenya/Kilifi/039/2015_05-Aug-2015	EPI_ISL_426153	Kilifi	6B.1	305,288	279,529	25.87	05-Aug-15
A/Kenya/Kilifi/040/2015_19-Aug-2015	EPI_ISL_426154	Kilifi	6B.1	427,875	409,540	23.79	19-Aug-15
A/Kenya/Kilifi/041/2015_18-Sep-2015	EPI_ISL_426155	Kilifi	6B.1	439,401	335,471	27.2	18-Sep-15
A/Kenya/Kilifi/043/2015_20-Sep-2015	EPI_ISL_426156	Kilifi	6B	423,787	414,836	23.75	20-Sep-15
A/Kenya/Kilifi/045/2015_15-Oct-2015	EPI_ISL_426157	Kilifi	6B.1	391,429	358,412	27.05	15-Oct-15
A/Kenya/Kilifi/047/2015_21-Nov-2015	EPI_ISL_426158	Kilifi	6B.1	486,930	443,085	26.19	21-Nov-15
A/Kenya/Kilifi/049/2015_25-Nov-2015	EPI_ISL_426162	Kilifi	6B.1	162,385	102,979	26.68	25-Nov-15

A/Kenya/Kilifi/127/2013_10-May-2013	EPI_ISL_426165	Kilifi	6C	297,138	283,777	22.98	10-May-13
A/Kenya/Kilifi/128/2013_26-Sep-2013	EPI_ISL_426170	Kilifi	6C	364,175	357,104	24.1	26-Sep-13
A/Kenya/Kilifi/134/2011_02-May-2011	EPI_ISL_426172	Kilifi	6	387,443	291,248	26.07	02-May-11
A/Kenya/Kilifi/137/2015_20-Aug-2015	EPI_ISL_426174	Kilifi	6B.1	448,709	38,958	27.04	20-Aug-15
A/Kenya/Kilifi/139/2015_01-Sep-2015	EPI_ISL_426175	Kilifi	6B	638,407	587,473	26.65	01-Sep-15
A/Kenya/Kilifi/150/2014_17-May-2014	EPI_ISL_426176	Kilifi	6B	497,822	399,792	29.2	17-May-14
A/Kenya/Kilifi/151/2014_27-May-2014	EPI_ISL_426177	Kilifi	6B	504,501	24,404	30.05	27-May-14
A/Kenya/Kilifi/153/2014_19-Jun-2014	EPI_ISL_426178	Kilifi	6B	645,749	424,306	31.67	19-Jun-14
A/Kenya/Kilifi/001/2018_12-Mar-2018	EPI_ISL_426329	Kilifi	6B.1A	304,202	294,730	24	12-Mar-18
A/Kenya/Kilifi/002/2018_24-Mar-2018	EPI_ISL_426330	Kilifi	6B.1A	307,214	255,618	29	24-Mar-18
A/Kenya/Kilifi/003/2018_26-Mar-2018	EPI_ISL_426331	Kilifi	6B.1A	500,713	429,745	29	26-Mar-18
A/Kenya/Kilifi/004/2018_13-Apr-2018	EPI_ISL_426332	Kilifi	6B.1A	356,989	131,635	29	13-Apr-18
A/Kenya/Kilifi/005/2018_14-Apr-2018	EPI_ISL_426333	Kilifi	6B.1A1	642,691	626,636	28	14-Apr-18
A/Kenya/Kilifi/007/2018_24-May-2018	EPI_ISL_426334	Kilifi	6B.1A	806,889	758,634	24	24-May-18
A/Kenya/Kilifi/008/2018_30-Jun-2018	EPI_ISL_426335	Kilifi	6B.1A	685,440	672,524	25	30-Jun-18
A/Kenya/Kilifi/009/2018_08-Jul-2018	EPI_ISL_426336	Kilifi	6B.1A	256,841	247,577	25	08-Jul-18
A/Kenya/Kilifi/010/2018_17-Jul-2018	EPI_ISL_426337	Kilifi	6B.1A1	278,113	97,139	34	17-Jul-18
A/Kenya/CDC-Mombasa/002/2018_16-Apr-2018	EPI_ISL_429838	Mombasa	6B.1A	365,933	268,588	29.1	16-Apr-18
A/Kenya/CDC-Mombasa/003/2018_16-Apr-2018	EPI_ISL_429839	Mombasa	6B.1A	238,363	152,998	27.6	16-Apr-18
A/Kenya/CDC-Mombasa/005/2018_13-Aug-2018	EPI_ISL_429840	Mombasa	6B.1A	91,463	28,413	26.53	13-Aug-18
A/Kenya/CDC-Mombasa/008/2018_29-May-2018	EPI_ISL_429841	Mombasa	6B.1A	116,618	17,889	32.56	29-May-18
A/Kenya/CDC-Mombasa/009/2018_10-Jul-2018	EPI_ISL_429842	Mombasa	6B.1A	232,086	7,852	29.53	10-Jul-18
A/Kenya/CDC-Kakamega/001/2009_20-Aug-2009	EPI_ISL_426338	Kakamega	7	389,432	362,682	21.8	20-Aug-09
A/Kenya/CDC-Kakamega/002/2009_21-Sep-2009	EPI_ISL_426339	Kakamega	7	292,111	102,495	25.24	21-Sep-09
A/Kenya/CDC-Kakamega/003/2009_21-Sep-2009	EPI_ISL_426340	Kakamega	7	398,530	376,771	35.84	21-Sep-09
A/Kenya/CDC-Kakamega/004/2009_21-Sep-2009	EPI_ISL_426341	Kakamega	7	362,863	319,140	21.54	21-Sep-09
A/Kenya/CDC-Kakamega/005/2009_27-Oct-2009	EPI_ISL_426342	Kakamega	7	401,755	371,725	18.3	27-Oct-09
A/Kenya/CDC-Kakamega/006/2009_07-Sep-2009	EPI_ISL_426343	Kakamega	7	416,971	393,168	20.75	07-Sep-09

A/Kenya/CDC-Kakamega/007/2009_21-Sep-2009	EPI_ISL_426344	Kakamega	7	369,029	214,113	23.22	21-Sep-09
A/Kenya/CDC-Kakamega/008/2009_21-Sep-2009	EPI_ISL_426345	Kakamega	7	418,683	380,595	20	21-Sep-09
A/Kenya/CDC-Kakamega/009/2009_21-Sep-2009	EPI_ISL_426346	Kakamega	7	359,524	239,692	29.35	21-Sep-09
A/Kenya/CDC-Kakamega/010/2009_21-Sep-2009	EPI_ISL_426347	Kakamega	7	273,384	255,038	21.86	21-Sep-09
A/Kenya/CDC-Kakamega/011/2009_21-Sep-2009	EPI_ISL_426348	Kakamega	7	169,321	135,974	25.08	21-Sep-09
A/Kenya/CDC-Kakamega/012/2009_11-Nov-2009	EPI_ISL_426349	Kakamega	7	259,304	223,602	22	11-Nov-09
A/Kenya/CDC-Kakamega/013/2009_09-Oct-2009	EPI_ISL_426350	Kakamega	7	239,758	160,794	20.98	09-Oct-09
A/Kenya/CDC-Kakamega/018/2009_22-Oct-2009	EPI_ISL_426351	Kakamega	7	245,738	233,259	20	22-Oct-09
A/Kenya/CDC-Kakamega/019/2009_22-Oct-2009	EPI_ISL_426352	Kakamega	7	336,502	302,637	21	22-Oct-09
A/Kenya/CDC-Kakamega/022/2009_04-Nov-2009	EPI_ISL_426353	Kakamega	7	316,845	195,410	20.6	04-Nov-09
A/Kenya/CDC-Kakamega/025/2009_10-Nov-2009	EPI_ISL_426354	Kakamega	7	386,000	111,846	23.53	10-Nov-09
A/Kenya/CDC-Kakamega/026/2009_30-Oct-2009	EPI_ISL_426355	Kakamega	7	388,093	353,408	23.14	30-Oct-09
A/Kenya/CDC-Kakamega/030/2010_08-Dec-2010	EPI_ISL_426486	Kakamega	6	199,391	98,009	21.11	08-Dec-10
A/Kenya/CDC-Kakamega/031/2010_29-Nov-2010	EPI_ISL_426487	Kakamega	6	213,127	185,147	22.75	29-Nov-10
A/Kenya/CDC-Kakamega/033/2011_17-Feb-2011	EPI_ISL_426488	Kakamega	6	462,944	394,470	23.05	17-Feb-11
A/Kenya/CDC-Kakamega/034/2011_21-Feb-2011	EPI_ISL_426489	Kakamega	6	361,977	294,698	20.83	21-Feb-11
A/Kenya/CDC-Kakamega/036/2011_24-Feb-2011	EPI_ISL_426490	Kakamega	6	484,795	147,591	28.77	24-Feb-11
A/Kenya/CDC-Kakamega/037/2011_24-Feb-2011	EPI_ISL_426491	Kakamega	6	403,695	374,222	23.14	24-Feb-11
A/Kenya/CDC-Kakamega/038/2011_25-Feb-2011	EPI_ISL_426492	Kakamega	6	384,397	364,242	20.58	25-Feb-11
A/Kenya/CDC-Kakamega/039/2011_28-Feb-2011	EPI_ISL_426493	Kakamega	6	269,901	9,872	32.05	28-Feb-11
A/Kenya/CDC-Kakamega/040/2011_01-Mar-2011	EPI_ISL_426494	Kakamega	6	324,077	312,399	18.56	01-Mar-11
A/Kenya/CDC-Kakamega/042/2011_03-Mar-2011	EPI_ISL_426570	Kakamega	6	329,934	305,769	18.42	03-Mar-11
A/Kenya/CDC-Kakamega/043/2011_04-Mar-2011	EPI_ISL_426571	Kakamega	6	342,351	329,426	17.26	04-Mar-11
A/Kenya/CDC-Kakamega/044/2011_07-Mar-2011	EPI_ISL_426572	Kakamega	6	424,142	157,680	25.31	07-Mar-11
A/Kenya/CDC-Kakamega/045/2011_08-Mar-2011	EPI_ISL_426573	Kakamega	6	456,243	422,644	23.09	08-Mar-11
A/Kenya/CDC-Kakamega/046/2011_08-Mar-2011	EPI_ISL_426574	Kakamega	6	396,884	371,515	21.36	08-Mar-11
A/Kenya/CDC-Kakamega/047/2011_14-Mar-2011	EPI_ISL_426575	Kakamega	6	348,177	320,253	20.87	14-Mar-11
A/Kenya/CDC-Kakamega/050/2011_25-Mar-2011	EPI_ISL_426576	Kakamega	6	388,372	357,204	24.06	25-Mar-11

A/Kenya/CDC-Kakamega/051/2011_26-Aug-2011	EPI_ISL_426577	Kakamega	6	440,336	377,618	22.89	26-Aug-11
A/Kenya/CDC-Kakamega/052/2011_06-Sep-2011	EPI_ISL_426578	Kakamega	6	386,323	148,215	27.03	06-Sep-11
A/Kenya/CDC-Kakamega/053/2011_01-Nov-2011	EPI_ISL_426579	Kakamega	6	380,427	61,460	24.6	01-Nov-11
A/Kenya/CDC-Kakamega/055/2014_04-Feb-2014	EPI_ISL_427399	Kakamega	6B	377,441	236,326	20.77	04-Feb-14
A/Kenya/CDC-Kakamega/056/2014_18-Mar-2014	EPI_ISL_427400	Kakamega	6B	403,934	330,681	24.2	18-Mar-14
A/Kenya/CDC-Kakamega/057/2014_31-Mar-2014	EPI_ISL_427401	Kakamega	6B	353,325	313,273	25.8	31-Mar-14
A/Kenya/CDC-Kakamega/060/2014_09-Jul-2014	EPI_ISL_427402	Kakamega	6B	366,009	337,683	21.47	09-Jul-14
A/Kenya/CDC-Kakamega/061/2014_05-Aug-2014	EPI_ISL_427403	Kakamega	6B	324,506	60,360	29.86	05-Aug-14
A/Kenya/CDC-Kakamega/062/2014_22-Sep-2014	EPI_ISL_427413	Kakamega	6B	341,420	316,186	29.09	22-Sep-14
A/Kenya/CDC-Kakamega/063/2014_24-Sep-2014	EPI_ISL_427421	Kakamega	6B	332,068	276,821	20.37	24-Sep-14
A/Kenya/CDC-Kakamega/064/2014_05-Nov-2014	EPI_ISL_427422	Kakamega	6B	360,160	201,660	28.06	05-Nov-14
A/Kenya/CDC-Kakamega/065/2014_17-Nov-2014	EPI_ISL_427423	Kakamega	6B	318,934	299,051	21.4	17-Nov-14
A/Kenya/CDC-Kakamega/066/2015_07-Apr-2015	EPI_ISL_427424	Kakamega	6B.1	403,221	382,165	26.4	07-Apr-15
A/Kenya/CDC-Kakamega/067/2016_18-Apr-2016	EPI_ISL_427425	Kakamega	6B.1	596,766	348,068	26.4	18-Apr-16
A/Kenya/CDC-Kakamega/068/2016_11-Jul-2016	EPI_ISL_427426	Kakamega	6B.1	472,521	412,151	27.1	11-Jul-16
A/Kenya/CDC-Kakamega/069/2016_19-Jul-2016	EPI_ISL_427463	Kakamega	6B.1	534,955	514,525	34.4	19-Jul-16
A/Kenya/CDC-Kakamega/070/2016_25-Jul-2016	EPI_ISL_427464	Kakamega	6B.1	367,029	243,584	25.7	25-Jul-16
A/Kenya/CDC-Kakamega/071/2016_10-Aug-2016	EPI_ISL_427465	Kakamega	6B.1	437,013	415,491	22.1	10-Aug-16
A/Kenya/CDC-Kakamega/072/2016_22-Aug-2016	EPI_ISL_427466	Kakamega	6B.1	253,195	112,244	26.9	22-Aug-16
A/Kenya/CDC-Kakamega/073/2016_22-Aug-2016	EPI_ISL_427467	Kakamega	6B.1	198,922	173,057	18.9	22-Aug-16
A/Kenya/CDC-Kakamega/075/2010_29-Nov-2010	EPI_ISL_427468	Kakamega	6	244,806	194,947	17.11	29-Nov-10
A/Kenya/CDC-Kakamega/076/2010_16-Dec-2010	EPI_ISL_427522	Kakamega	7	379,381	186,375	23.86	16-Dec-10
A/Kenya/CDC-Kakamega/077/2010_04-Nov-2010	EPI_ISL_427523	Kakamega	6	155,754	101,659	20.29	04-Nov-10
A/Kenya/CDC-Kakamega/001/2018_04-Apr-2018	EPI_ISL_428406	Kakamega	6B.1A	514,088	371,044	22.27	04-Apr-18
A/Kenya/CDC-Kakamega/002/2018_27-Aug-2018	EPI_ISL_428407	Kakamega	6B.1A	326,275	196,839	27.16	27-Aug-18
A/Kenya/CDC-Kakamega/003/2018_01-Aug-2018	EPI_ISL_428408	Kakamega	6B.1A	354,069	112,377	32.66	01-Aug-18
A/Kenya/CDC-Kakamega/004/2018_30-Jul-2018	EPI_ISL_428409	Kakamega	6B.1A	427,916	134,909	28.75	30-Jul-18
A/Kenya/CDC-Kakamega/005/2018_30-Jul-2018	EPI_ISL_428410	Kakamega	6B.1A	411,686	309,308	29.18	30-Jul-18

A/Kenya/CDC-Kakamega/006/2018_27-Mar-2018	EPI_ISL_428411	Kakamega	6B.1A	479,623	355,621	24.08	27-Mar-18
A/Kenya/CDC-Kakamega/007/2018_12-Jun-2018	EPI_ISL_428412	Kakamega	6B.1A	589,366	154,895	22.34	12-Jun-18
A/Kenya/CDC-Kakamega/008/2018_26-Jun-2018	EPI_ISL_428413	Kakamega	6B.1A	381,724	1,143	30.16	26-Jun-18
A/Kenya/CDC-Kakamega/009/2018_29-May-2018	EPI_ISL_428414	Kakamega	6B.1A	470,390	135,158	32.6	29-May-18
A/Kenya/CDC-Kakamega/010/2018_16-Jul-2018	EPI_ISL_428415	Kakamega	6B.1A	352,581	268,409	23.42	16-Jul-18
A/Kenya/CDC-Kakamega/014/2018_16-Jul-2018	EPI_ISL_428416	Kakamega	6B.1A	299,782	51,368	28.23	16-Jul-18
A/Kenya/CDC-Kakamega/015/2018_24-Jul-2018	EPI_ISL_428417	Kakamega	6B.1A	163,080	95,491	29.17	24-Jul-18
A/Kenya/CDC-Kakamega/017/2018_03-Jul-2018	EPI_ISL_428418	Kakamega	6B.1A	384,768	207,379	22.85	03-Jul-18
A/Kenya/CDC-Kakamega/018/2018_03-Jul-2018	EPI_ISL_428419	Kakamega	6B.1A	328,555	220,877	24.98	03-Jul-18
A/Kenya/CDC-KNH/001/2009_10-Jul-2009	EPI_ISL_420557	Nairobi	7	356,713	203,327	23.47	10-Jul-09
A/Kenya/CDC-KNH/002/2009_23-Jul-2009	EPI_ISL_420558	Nairobi	7	307,112	264,747	16.4	23-Jul-09
A/Kenya/CDC-KNH/003/2009_29-Jul-2009	EPI_ISL_420559	Nairobi	7	279,794	250,552	17.1	29-Jul-09
A/Kenya/CDC-KNH/004/2009_11-Aug-2009	EPI_ISL_420560	Nairobi	7	355,997	138,759	27.9	11-Aug-09
A/Kenya/CDC-KNH/006/2009_12-Oct-2009	EPI_ISL_420561	Nairobi	7	512,867	477,635	20.19	12-Oct-09
A/Kenya/CDC-KNH/009/2009_03-Nov-2009	EPI_ISL_420562	Nairobi	7	413,095	237,635	21.19	03-Nov-09
A/Kenya/CDC-KNH/011/2009_25-Nov-2009	EPI_ISL_420593	Nairobi	7	510,128	401,176	24.44	25-Nov-09
A/Kenya/CDC-KNH/012/2009_27-Nov-2009	EPI_ISL_420594	Nairobi	7	459,359	150,578	27.48	27-Nov-09
A/Kenya/CDC-KNH/013/2009_30-Nov-2009	EPI_ISL_420595	Nairobi	7	262,594	112,063	26.39	30-Nov-09
A/Kenya/CDC-KNH/014/2009_02-Dec-2009	EPI_ISL_420596	Nairobi	7	376,127	346,849	17.76	02-Dec-09
A/Kenya/CDC-KNH/021/2010_09-Nov-2010	EPI_ISL_420597	Nairobi	6	329,325	272,269	27.21	09-Nov-10
A/Kenya/CDC-KNH/022/2010_10-Nov-2010	EPI_ISL_420601	Nairobi	6	272,030	162,259	25.49	10-Nov-10
A/Kenya/CDC-KNH/023/2010_10-Nov-2010	EPI_ISL_420602	Nairobi	6	327,253	290,985	22.41	10-Nov-10
A/Kenya/CDC-KNH/024/2010_11-Nov-2010	EPI_ISL_420603	Nairobi	6	281,273	172,972	20.5	11-Nov-10
A/Kenya/CDC-KNH/025/2010_17-Nov-2010	EPI_ISL_420626	Nairobi	7	239,229	18,423	29	17-Nov-10
A/Kenya/CDC-KNH/026/2010_17-Nov-2010	EPI_ISL_420627	Nairobi	7	231,176	122,567	28.03	17-Nov-10
A/Kenya/CDC-KNH/028/2010_23-Nov-2010	EPI_ISL_420778	Nairobi	6	293,572	34,469	27.55	23-Nov-10
A/Kenya/CDC-KNH/029/2010_23-Nov-2010	EPI_ISL_420779	Nairobi	6	249,235	200,995	23.85	23-Nov-10
A/Kenya/CDC-KNH/030/2010_29-Nov-2010	EPI_ISL_420780	Nairobi	6	428,048	96,991	26.88	29-Nov-10

A/Kenya/CDC-KNH/031/2010_30-Nov-2010	EPI_ISL_420781	Nairobi	6	205,607	158,004	21.76	30-Nov-10
A/Kenya/CDC-KNH/032/2010_07-Dec-2010	EPI_ISL_420782	Nairobi	6	272,638	237,512	39.7	07-Dec-10
A/Kenya/CDC-KNH/033/2010_10-Dec-2010	EPI_ISL_420783	Nairobi	6	353,662	246,376	27.31	10-Dec-10
A/Kenya/CDC-KNH/034/2011_14-Mar-2011	EPI_ISL_420826	Nairobi	6	423,169	148,427	27	14-Mar-11
A/Kenya/CDC-KNH/035/2011_21-Feb-2011	EPI_ISL_420827	Nairobi	6	305,802	162,181	21.95	21-Feb-11
A/Kenya/CDC-KNH/038/2011_23-Feb-2011	EPI_ISL_420828	Nairobi	6	295,100	107,609	19.52	23-Feb-11
A/Kenya/CDC-KNH/040/2011_23-May-2011	EPI_ISL_420829	Nairobi	6	281,968	48,074	24.04	23-May-11
A/Kenya/CDC-KNH/043/2011_23-Jun-2011	EPI_ISL_420830	Nairobi	6	271,642	211,103	21.07	23-Jun-11
A/Kenya/CDC-KNH/044/2011_29-Jun-2011	EPI_ISL_420831	Nairobi	6	232,122	131,817	22.05	29-Jun-11
A/Kenya/CDC-KNH/045/2011_29-Jun-2011	EPI_ISL_420832	Nairobi	6	321,517	258,677	22.38	29-Jun-11
A/Kenya/CDC-KNH/046/2011_05-Jul-2011	EPI_ISL_420833	Nairobi	6	601,661	529,348	23.04	05-Jul-11
A/Kenya/CDC-KNH/047/2011_07-Jul-2011	EPI_ISL_420834	Nairobi	6	314,224	138,817	22.72	07-Jul-11
A/Kenya/CDC-KNH/048/2011_08-Jul-2011	EPI_ISL_420835	Nairobi	6	370,051	347,452	21.91	08-Jul-11
A/Kenya/CDC-KNH/049/2011_11-Jul-2011	EPI_ISL_420836	Nairobi	6	256,284	89,658	23.55	11-Jul-11
A/Kenya/CDC-KNH/050/2011_12-Jul-2011	EPI_ISL_420837	Nairobi	6	297,063	191,273	23.55	12-Jul-11
A/Kenya/CDC-KNH/051/2011_12-Jul-2011	EPI_ISL_420880	Nairobi	6	215,010	75,746	26.16	12-Jul-11
A/Kenya/CDC-KNH/052/2011_14-Jul-2011	EPI_ISL_420881	Nairobi	6	271,297	236,004	22.87	14-Jul-11
A/Kenya/CDC-KNH/053/2011_14-Jul-2011	EPI_ISL_420882	Nairobi	6	302,890	191,905	25.45	14-Jul-11
A/Kenya/CDC-KNH/054/2011_14-Jul-2011	EPI_ISL_421216	Nairobi	6	327,353	283,127	20.97	14-Jul-11
A/Kenya/CDC-KNH/055/2011_19-Jul-2011	EPI_ISL_421217	Nairobi	6	324,232	303,460	20.08	19-Jul-11
A/Kenya/CDC-KNH/056/2011_21-Jul-2011	EPI_ISL_421218	Nairobi	6	292,784	255,909	25.27	21-Jul-11
A/Kenya/CDC-KNH/057/2011_22-Jul-2011	EPI_ISL_421219	Nairobi	6	327,137	300,731	23.54	22-Jul-11
A/Kenya/CDC-KNH/058/2011_22-Jul-2011	EPI_ISL_421220	Nairobi	6	273,532	214,309	23.92	22-Jul-11
A/Kenya/CDC-KNH/061/2011_05-Aug-2011	EPI_ISL_421255	Nairobi	6	248,738	133,214	25.46	05-Aug-11
A/Kenya/CDC-KNH/062/2011_08-Aug-2011	EPI_ISL_421263	Nairobi	6	302,353	199,603	25.3	08-Aug-11
A/Kenya/CDC-KNH/063/2011_10-Aug-2011	EPI_ISL_421265	Nairobi	6	294,700	220,301	27.18	10-Aug-11
A/Kenya/CDC-KNH/065/2011_01-Sep-2011	EPI_ISL_421266	Nairobi	6	215,341	162,201	22.27	01-Sep-11
A/Kenya/CDC-KNH/066/2011_12-Oct-2011	EPI_ISL_421270	Nairobi	7	247,941	11,900	32.02	12-Oct-11

A/Kenya/CDC-KNH/067/2011_19-Oct-2011	EPI_ISL_421271	Nairobi	7	214,945	6,036	29.23	19-Oct-11
A/Kenya/CDC-KNH/070/2014_12-Feb-2014	EPI_ISL_421274	Nairobi	6B	425,136	407,057	25.72	12-Feb-14
A/Kenya/CDC-KNH/071/2014_27-Feb-2014	EPI_ISL_421276	Nairobi	6B	372,750	339,494	24.81	27-Feb-14
A/Kenya/CDC-KNH/080/2015_16-Jul-2015	EPI_ISL_421278	Nairobi	6B.1	209,728	153,253	20.88	16-Jul-15
A/Kenya/CDC-KNH/081/2015_21-Jul-2015	EPI_ISL_421277	Nairobi	6B.1	266,668	60,902	25.69	21-Jul-15
A/Kenya/CDC-KNH/084/2015_05-Aug-2015	EPI_ISL_421280	Nairobi	6B.1	208,305	51,388	24.55	05-Aug-15
A/Kenya/CDC-KNH/085/2015_11-Aug-2015	EPI_ISL_421282	Nairobi	6B.1	234,582	96,796	24.17	11-Aug-15
A/Kenya/CDC-KNH/088/2015_03-Sep-2015	EPI_ISL_421337	Nairobi	6B.1	292,273	261,866	21.08	03-Sep-15
A/Kenya/CDC-KNH/089/2016_04-Jul-2016	EPI_ISL_421344	Nairobi	6B.1	246,192	57,212	21.94	04-Jul-16
A/Kenya/CDC-KNH/002/2018_22-Jan-2018	EPI_ISL_421436	Nairobi	6B.1A	497,508	372,878	23	22-Jan-18
A/Kenya/CDC-KNH/004/2018_20-Feb-2018	EPI_ISL_421437	Nairobi	6B.1A	487,180	245,593	27.3	20-Feb-18
A/Kenya/CDC-KNH/005/2018_19-Feb-2018	EPI_ISL_421438	Nairobi	6B.1A	341,749	79,956	29.2	19-Feb-18
A/Kenya/CDC-KNH/008/2018_26-Feb-2018	EPI_ISL_421439	Nairobi	6B.1A	366,823	244,725	24.6	26-Feb-18
A/Kenya/CDC-KNH/009/2018_19-Mar-2018	EPI_ISL_421440	Nairobi	6B.1A	289,682	185,392	24.01	19-Mar-18
A/Kenya/CDC-KNH/010/2018_17-Apr-2018	EPI_ISL_421441	Nairobi	6B.1A	267,659	195,654	20.7	17-Apr-18
A/Kenya/CDC-KNH/011/2018_20-Mar-2018	EPI_ISL_421442	Nairobi	6B.1A	602,558	251,805	29.2	20-Mar-18
A/Kenya/CDC-KNH/014/2018_04-Apr-2018	EPI_ISL_421443	Nairobi	6B.1A	271,997	191,486	23.41	04-Apr-18
A/Kenya/CDC-KNH/015/2018_04-Apr-2018	EPI_ISL_421444	Nairobi	6B.1A	329,256	162,570	28.57	04-Apr-18
A/Kenya/CDC-KNH/016/2018_10-Apr-2018	EPI_ISL_421445	Nairobi	6B.1A	183,133	73,945	24.4	10-Apr-18
A/Kenya/CDC-Nakuru/004/2011_02-Nov-2011	EPI_ISL_421522	Nakuru	7	383,458	234,498	27.7	02-Nov-11
A/Kenya/CDC-Nakuru/005/2012_20-Mar-2012	EPI_ISL_421523	Nakuru	7	510,935	408,606	21.77	20-Mar-12
A/Kenya/CDC-Nakuru/009/2013_22-Jan-2013	EPI_ISL_421524	Nakuru	6C	242,999	69,076	27.31	22-Jan-13
A/Kenya/CDC-Nakuru/010/2013_25-Mar-2013	EPI_ISL_421525	Nakuru	6C	380,142	163,960	21.65	25-Mar-13
A/Kenya/CDC-Nakuru/011/2013_27-Mar-2013	EPI_ISL_421526	Nakuru	6C	312,634	115,301	25.2	27-Mar-13
A/Kenya/CDC-Nakuru/012/2014_22-Jan-2014	EPI_ISL_421527	Nakuru	6C	294,204	38,310	23.77	22-Jan-14
A/Kenya/CDC-Nakuru/013/2014_17-Mar-2014	EPI_ISL_421528	Nakuru	6B	416,492	242,552	21.44	17-Mar-14
A/Kenya/CDC-Nakuru/014/2014_24-Mar-2014	EPI_ISL_421529	Nakuru	6B	222,722	164,302	22.5	24-Mar-14
A/Kenya/CDC-Nakuru/016/2014_08-Apr-2014	EPI_ISL_421530	Nakuru	6B	255,510	207,152	17.3	08-Apr-14

A/Kenya/CDC-Nakuru/017/2014_15-Apr-2014	EPI_ISL_421532	Nakuru	6B	444,216	302,230	17.3	15-Apr-14
A/Kenya/CDC-Nakuru/018/2014_05-May-2014	EPI_ISL_421533	Nakuru	6B	576,740	393,795	22.5	05-May-14
A/Kenya/CDC-Nakuru/019/2014_28-May-2014	EPI_ISL_421534	Nakuru	6B	296,433	112,500	21.2	28-May-14
A/Kenya/CDC-Nakuru/020/2014_03-Jun-2014	EPI_ISL_421535	Nakuru	6B	534,806	347,332	21	03-Jun-14
A/Kenya/CDC-Nakuru/021/2014_11-Jun-2014	EPI_ISL_421536	Nakuru	6B	257,203	12,831	23.13	11-Jun-14
A/Kenya/CDC-Nakuru/022/2014_18-Jun-2014	EPI_ISL_421537	Nakuru	6B	740,135	537,318	18.2	18-Jun-14
A/Kenya/CDC-Nakuru/023/2014_23-Jun-2014	EPI_ISL_421538	Nakuru	6B	349,425	230,576	21	23-Jun-14
A/Kenya/CDC-Nakuru/024/2014_30-Jun-2014	EPI_ISL_421339	Nakuru	6B	489,810	344,759	23.7	30-Jun-14
A/Kenya/CDC-Nakuru/025/2014_01-Jul-2014	EPI_ISL_421540	Nakuru	6B	359,707	22,099	22.7	01-Jul-14
A/Kenya/CDC-Nakuru/026/2014_02-Jul-2014	EPI_ISL_421541	Nakuru	6B	487,811	307,039	29.2	02-Jul-14
A/Kenya/CDC-Nakuru/027/2014_09-Jul-2014	EPI_ISL_421542	Nakuru	6B	354,921	301,049	25.23	09-Jul-14
A/Kenya/CDC-Nakuru/028/2014_14-Jul-2014	EPI_ISL_421555	Nakuru	6B	439,664	385,973	21.58	14-Jul-14
A/Kenya/CDC-Nakuru/029/2014_15-Jul-2014	EPI_ISL_421556	Nakuru	6B	375,662	178,254	25.6	15-Jul-14
A/Kenya/CDC-Nakuru/030/2014_21-Jul-2014	EPI_ISL_421557	Nakuru	6B	410,708	117,211	24.4	21-Jul-14
A/Kenya/CDC-Nakuru/031/2014_22-Jul-2014	EPI_ISL_421558	Nakuru	6B	396,869	262,004	20.86	22-Jul-14
A/Kenya/CDC-Nakuru/032/2015_27-Apr-2015	EPI_ISL_421559	Nakuru	6B.1	449,900	166,848	23.49	27-Apr-15
A/Kenya/CDC-Nakuru/034/2015_20-Jul-2015	EPI_ISL_421564	Nakuru	6B.1	467,881	109,317	24.55	20-Jul-15
A/Kenya/CDC-Nakuru/037/2015_28-Jul-2015	EPI_ISL_421565	Nakuru	6B.1	360,552	303,957	23.8	28-Jul-15
A/Kenya/CDC-Nakuru/039/2015_03-Aug-2015	EPI_ISL_421566	Nakuru	6B.1	695,550	623,746	25.5	03-Aug-15
A/Kenya/CDC-Nakuru/040/2015_05-Aug-2015	EPI_ISL_421567	Nakuru	6B.1	348,475	311,170	17.4	05-Aug-15
A/Kenya/CDC-Nakuru/041/2015_05-Aug-2015	EPI_ISL_421568	Nakuru	6B.1	445,802	360,430	26.6	05-Aug-15
A/Kenya/CDC-Nakuru/042/2015_10-Aug-2015	EPI_ISL_421569	Nakuru	6B.1	238,086	197,175	25.4	10-Aug-15
A/Kenya/CDC-Nakuru/043/2015_18-Aug-2015	EPI_ISL_421570	Nakuru	6B.1	395,520	270,678	26.3	18-Aug-15
A/Kenya/CDC-Nakuru/044/2015_11-Nov-2015	EPI_ISL_421571	Nakuru	6B.1	231,569	90,709	25.8	11-Nov-15
A/Kenya/CDC-Nakuru/045/2016_15-Feb-2016	EPI_ISL_421657	Nakuru	6B.1	605,757	493,016	23.97	15-Feb-16
A/Kenya/CDC-Nakuru/046/2016_02-Apr-2016	EPI_ISL_421658	Nakuru	6B.1	865,073	700,744	21.99	02-Apr-16
A/Kenya/CDC-Nakuru/047/2016_30-Mar-2016	EPI_ISL_421659	Nakuru	6B.1	604,254	521,496	17.2	30-Mar-16
A/Kenya/CDC-Nakuru/050/2016_06-Apr-2016	EPI_ISL_421661	Nakuru	6B.1	684,147	610,152	25.4	06-Apr-16

A/Kenya/CDC-Nakuru/051/2016_08-Apr-2016	EPI_ISL_421673	Nakuru	6B.1	567,374	450,818	22.8	08-Apr-16
A/Kenya/CDC-Nakuru/052/2016_13-Apr-2016	EPI_ISL_421674	Nakuru	6B.1	359,934	22,170	25.8	13-Apr-16
A/Kenya/CDC-Nakuru/054/2010_11-Aug-2010	EPI_ISL_421676	Nakuru	7	317,922	144,366	18.9	11-Aug-10
A/Kenya/CDC-Nakuru/055/2010_11-Aug-2010	EPI_ISL_421677	Nakuru	7	414,528	367,359	20.98	11-Aug-10
A/Kenya/CDC-Nakuru/056/2010_12-Oct-2010	EPI_ISL_421678	Nakuru	6	325,213	176,771	24.3	12-Oct-10
A/Kenya/CDC-Nakuru/058/2010_18-Oct-2010	EPI_ISL_421679	Nakuru	6	306,288	227,581	26.52	18-Oct-10
A/Kenya/CDC-Nakuru/060/2010_25-Oct-2010	EPI_ISL_421680	Nakuru	6	433,497	257,779	22.13	25-Oct-10
A/Kenya/CDC-Nakuru/061/2010_29-Oct-2010	EPI_ISL_421681	Nakuru	6	377,727	171,987	23.76	29-Oct-10
A/Kenya/CDC-Nakuru/062/2010_23-Jul-2010	EPI_ISL_421682	Nakuru	7	393,022	305,512	23	23-Jul-10
A/Kenya/CDC-Nakuru/063/2010_05-Nov-2010	EPI_ISL_421693	Nakuru	6	442,725	361,079	25.99	05-Nov-10
A/Kenya/CDC-Nakuru/065/2010_12-Oct-2010	EPI_ISL_421694	Nakuru	6	297,710	178,654	23.05	12-Oct-10
A/Kenya/CDC-Nakuru/067/2010_12-Oct-2010	EPI_ISL_421695	Nakuru	6	362,506	305,527	25.68	12-Oct-10
A/Kenya/CDC-Nakuru/068/2010_15-Oct-2010	EPI_ISL_421696	Nakuru	6	482,688	403,114	19.59	15-Oct-10
A/Kenya/CDC-Nakuru/069/2010_17-Nov-2010	EPI_ISL_421697	Nakuru	6	505,039	327,212	25.56	17-Nov-10
A/Kenya/CDC-Nakuru/071/2010_24-Nov-2010	EPI_ISL_421698	Nakuru	6	481,856	443,359	24.63	24-Nov-10
A/Kenya/CDC-Nakuru/072/2010_24-Nov-2010	EPI_ISL_421699	Nakuru	7	362,328	113,065	23.28	24-Nov-10
A/Kenya/CDC-Nakuru/073/2010_25-Nov-2010	EPI_ISL_421700	Nakuru	7	200,394	70,325	29.22	25-Nov-10
A/Kenya/CDC-Nakuru/074/2010_25-Nov-2010	EPI_ISL_421701	Nakuru	6	275,763	21,602	25.37	25-Nov-10
A/Kenya/CDC-Nakuru/076/2010_01-Dec-2010	EPI_ISL_421702	Nakuru	7	503,775	210,290	26.94	01-Dec-10
A/Kenya/CDC-Nakuru/077/2010_02-Dec-2010	EPI_ISL_421703	Nakuru	7	366,783	200,568	28.05	02-Dec-10
A/Kenya/CDC-Nakuru/078/2009_28-Oct-2009	EPI_ISL_421764	Nakuru	7	416,485	282,773	18.6	28-Oct-09
A/Kenya/CDC-Nakuru/079/2009_29-Oct-2009	EPI_ISL_421765	Nakuru	7	280,671	188,073	24.02	29-Oct-09
A/Kenya/CDC-Nakuru/080/2009_02-Nov-2009	EPI_ISL_421766	Nakuru	7	352,235	285,019	24.7	02-Nov-09
A/Kenya/CDC-Nakuru/081/2009_03-Nov-2009	EPI_ISL_421767	Nakuru	7	377,915	319,787	17.1	03-Nov-09
A/Kenya/CDC-Nakuru/083/2009_26-Oct-2009	EPI_ISL_421950	Nakuru	7	265,629	181,183	21.6	26-Oct-09
A/Kenya/CDC-Nakuru/084/2009_04-Nov-2009	EPI_ISL_422013	Nakuru	7	236,068	189,672	20.8	04-Nov-09
A/Kenya/CDC-Nakuru/086/2009_06-Nov-2009	EPI_ISL_422014	Nakuru	7	261,635	222,463	21.8	06-Nov-09
A/Kenya/CDC-Nakuru/087/2009_09-Nov-2009	EPI_ISL_422015	Nakuru	7	409,263	355,435	18.7	09-Nov-09

A/Kenya/CDC-Nakuru/088/2009_10-Nov-2009	EPI_ISL_422101	Nakuru	7	435,204	373,874	19.4	10-Nov-09
A/Kenya/CDC-Nakuru/089/2009_10-Nov-2009	EPI_ISL_422367	Nakuru	7	310,712	233,112	22.2	10-Nov-09
A/Kenya/CDC-Nakuru/090/2009_10-Nov-2009	EPI_ISL_422378	Nakuru	7	331,088	178,755	21.7	10-Nov-09
A/Kenya/CDC-Nakuru/091/2009_13-Nov-2009	EPI_ISL_422379	Nakuru	7	210,474	84,637	21.5	13-Nov-09
A/Kenya/CDC-Nakuru/093/2009_16-Nov-2009	EPI_ISL_422380	Nakuru	7	260,183	76,832	20.4	16-Nov-09
A/Kenya/CDC-Nakuru/094/2009_17-Nov-2009	EPI_ISL_422381	Nakuru	7	275,244	204,809	21.7	17-Nov-09
A/Kenya/CDC-Nakuru/095/2011_24-Mar-2011	EPI_ISL_422452	Nakuru	6	188,229	74,027	21.29	24-Mar-11
A/Kenya/CDC-Nakuru/096/2011_24-Nov-2011	EPI_ISL_422454	Nakuru	6	248,482	119,169	29	24-Nov-11
A/Kenya/CDC-Nakuru/097/2011_24-Nov-2011	EPI_ISL_422455	Nakuru	6	334,834	276,076	30.5	24-Nov-11
A/Kenya/CDC-Nakuru/098/2011_27-Jun-2011	EPI_ISL_422456	Nakuru	6	328,150	174,718	26.79	27-Jun-11
A/Kenya/CDC-Nakuru/099/2011_28-Jun-2011	EPI_ISL_422457	Nakuru	6	253,837	146,841	19.9	28-Jun-11
A/Kenya/CDC-Nakuru/100/2011_11-Jul-2011	EPI_ISL_422458	Nakuru	6	194,350	7,890	27	11-Jul-11
A/Kenya/CDC-Nakuru/103/2011_22-Mar-2011	EPI_ISL_422460	Nakuru	6	331,464	289,809	24.72	22-Mar-11
A/Kenya/CDC-Nakuru/104/2011_05-Apr-2011	EPI_ISL_422466	Nakuru	6	763,464	712,514	17.5	05-Apr-11
A/Kenya/CDC-Nakuru/105/2011_20-Jun-2011	EPI_ISL_422467	Nakuru	6	339,321	217,897	21.48	20-Jun-11
A/Kenya/CDC-Nakuru/106/2011_27-Jun-2011	EPI_ISL_422468	Nakuru	6	454,344	327,687	21.7	27-Jun-11
A/Kenya/CDC-Nakuru/107/2011_28-Jun-2011	EPI_ISL_422469	Nakuru	6	454,061	389,001	17.37	28-Jun-11
A/Kenya/CDC-Nakuru/110/2011_18-Oct-2011	EPI_ISL_422470	Nakuru	7	429,964	371,238	20.6	18-Oct-11
A/Kenya/CDC-Nakuru/112/2011_18-Nov-2011	EPI_ISL_422471	Nakuru	6	451,047	374,721	19.1	18-Nov-11
A/Kenya/CDC-Nakuru/001/2018_23-Apr-2018	EPI_ISL_422472	Nakuru	6B.1A	294,829	159,849	23.2	23-Apr-18
A/Kenya/CDC-Nakuru/002/2018_24-Jul-2018	EPI_ISL_422473	Nakuru	6B.1A	327,716	178,329	29.94	24-Jul-18
A/Kenya/CDC-Nakuru/003/2018_13-Mar-2018	EPI_ISL_422474	Nakuru	6B.1A	366,650	256,545	26.22	13-Mar-18
A/Kenya/CDC-Nakuru/004/2018_03-Apr-2018	EPI_ISL_422475	Nakuru	6B.1A	199,097	134,067	23.1	03-Apr-18
A/Kenya/CDC-Nakuru/005/2018_03-Apr-2018	EPI_ISL_422476	Nakuru	6B.1A	309,325	162,079	22.6	03-Apr-18
A/Kenya/CDC-Nakuru/006/2018_03-Apr-2018	EPI_ISL_422477	Nakuru	6B.1A	525,695	191,036	24.7	03-Apr-18
A/Kenya/CDC-Nakuru/010/2018_11-Jun-2018	EPI_ISL_422478	Nakuru	6B.1A	221,586	159,411	29.92	11-Jun-18
A/Kenya/CDC-Nakuru/011/2018_30-Jul-2018	EPI_ISL_422479	Nakuru	6B.1A	178,665	5,425	32.82	30-Jul-18
A/Kenya/CDC-Nakuru/012/2018_27-Jun-2018	EPI_ISL_422480	Nakuru	6B.1A	293,737	20,318	29.71	27-Jun-18

A/Kenya/CDC-Nakuru/013/2018_21-May-2018	EPI_ISL_422481	Nakuru	6B.1A	429,890	308,684	24.8	21-May-18
A/Kenya/CDC-Nakuru/014/2018_11-Apr-2018	EPI_ISL_422482	Nakuru	6B.1A	264,748	133,709	25.2	11-Apr-18
A/Kenya/CDC-Nakuru/016/2018_18-Jul-2018	EPI_ISL_422483	Nakuru	6B.1A	299,643	214,617	33.61	18-Jul-18
A/Kenya/CDC-Nakuru/018/2018_05-Mar-2018	EPI_ISL_422484	Nakuru	6B.1A	228,310	127,356	21.5	05-Mar-18
A/Kenya/CDC-Nakuru/019/2018_05-Mar-2018	EPI_ISL_422485	Nakuru	6B.1A	497,738	366,541	25.37	05-Mar-18
A/Kenya/CDC-Nakuru/021/2018_03-Jul-2018	EPI_ISL_422486	Nakuru	6B.1A	424,404	279,347	24.33	03-Jul-18
A/Kenya/CDC-Nakuru/022/2018_07-May-2018	EPI_ISL_422487	Nakuru	6B.1A	216,098	13,847	29.4	07-May-18
A/Kenya/CDC-Nyeri/001/2009_12-Aug-2009	EPI_ISL_428733	Nyeri	7	435,226	311,675	25.9	12-Aug-09
A/Kenya/CDC-Nyeri/002/2009_03-Sep-2009	EPI_ISL_428734	Nyeri	7	369,437	332,785	21.22	03-Sep-09
A/Kenya/CDC-Nyeri/003/2009_03-Sep-2009	EPI_ISL_428735	Nyeri	7	337,521	302,402	23.54	03-Sep-09
A/Kenya/CDC-Nyeri/004/2009_28-Sep-2009	EPI_ISL_428736	Nyeri	7	389,988	326,235	20.59	28-Sep-09
A/Kenya/CDC-Nyeri/006/2009_21-Oct-2009	EPI_ISL_428737	Nyeri	7	220,409	197,402	18.3	21-Oct-09
A/Kenya/CDC-Nyeri/007/2009_22-Oct-2009	EPI_ISL_428738	Nyeri	7	333,776	257,906	27.3	22-Oct-09
A/Kenya/CDC-Nyeri/010/2009_04-Nov-2009	EPI_ISL_428739	Nyeri	7	325,501	217,456	24.1	04-Nov-09
A/Kenya/CDC-Nyeri/011/2009_05-Nov-2009	EPI_ISL_428741	Nyeri	7	376,182	336,265	22.8	05-Nov-09
A/Kenya/CDC-Nyeri/012/2009_06-Nov-2009	EPI_ISL_428742	Nyeri	7	326,130	273,495	21.7	06-Nov-09
A/Kenya/CDC-Nyeri/014/2009_10-Nov-2009	EPI_ISL_428743	Nyeri	7	340,468	180,346	25.44	10-Nov-09
A/Kenya/CDC-Nyeri/016/2009_13-Nov-2009	EPI_ISL_428744	Nyeri	7	255,056	190,694	25.8	13-Nov-09
A/Kenya/CDC-Nyeri/017/2009_16-Nov-2009	EPI_ISL_428753	Nyeri	7	411,801	248,076	21.5	16-Nov-09
A/Kenya/CDC-Nyeri/018/2009_20-Nov-2009	EPI_ISL_428754	Nyeri	7	327,102	222,283	22.43	20-Nov-09
A/Kenya/CDC-Nyeri/019/2009_02-Dec-2009	EPI_ISL_428755	Nyeri	7	291,812	34,172	22.62	02-Dec-09
A/Kenya/CDC-Nyeri/020/2009_09-Dec-2009	EPI_ISL_428756	Nyeri	7	257,950	92,255	24.23	09-Dec-09
A/Kenya/CDC-Nyeri/021/2010_18-Jun-2010	EPI_ISL_428806	Nyeri	7	389,613	326,008	18.72	18-Jun-10
A/Kenya/CDC-Nyeri/022/2010_22-Jun-2010	EPI_ISL_428807	Nyeri	7	361,105	170,412	24.88	22-Jun-10
A/Kenya/CDC-Nyeri/023/2010_24-Jun-2010	EPI_ISL_428808	Nyeri	7	325,727	171,080	22.31	24-Jun-10
A/Kenya/CDC-Nyeri/024/2010_09-Jul-2010	EPI_ISL_428809	Nyeri	7	371,807	148,319	20.42	09-Jul-10
A/Kenya/CDC-Nyeri/025/2010_20-Jul-2010	EPI_ISL_428810	Nyeri	7	310,207	99,677	21.61	20-Jul-10
A/Kenya/CDC-Nyeri/026/2010_26-Jul-2010	EPI_ISL_428811	Nyeri	7	332,666	185,118	21.33	26-Jul-10

A/Kenya/CDC-Nyeri/027/2010_27-Jul-2010	EPI_ISL_428812	Nyeri	7	288,267	114,315	25	27-Jul-10
A/Kenya/CDC-Nyeri/028/2010_29-Jul-2010	EPI_ISL_428813	Nyeri	7	278,641	49,237	21.3	29-Jul-10
A/Kenya/CDC-Nyeri/031/2010_17-Sep-2010	EPI_ISL_428814	Nyeri	6	227,794	170,469	20.3	17-Sep-10
A/Kenya/CDC-Nyeri/032/2010_18-Oct-2010	EPI_ISL_428815	Nyeri	6	384,905	324,018	21.02	18-Oct-10
A/Kenya/CDC-Nyeri/033/2010_22-Oct-2010	EPI_ISL_428816	Nyeri	6	312,191	280,454	23.1	22-Oct-10
A/Kenya/CDC-Nyeri/034/2010_09-Nov-2010	EPI_ISL_428817	Nyeri	6	433,594	262,599	21.59	09-Nov-10
A/Kenya/CDC-Nyeri/035/2010_10-Nov-2010	EPI_ISL_428818	Nyeri	7	405,017	204,824	21.54	10-Nov-10
A/Kenya/CDC-Nyeri/036/2010_15-Nov-2010	EPI_ISL_428819	Nyeri	6	352,763	195,517	22.32	15-Nov-10
A/Kenya/CDC-Nyeri/037/2011_04-Jan-2011	EPI_ISL_428933	Nyeri	6	389,528	217,418	23.21	04-Jan-11
A/Kenya/CDC-Nyeri/038/2011_14-Feb-2011	EPI_ISL_428934	Nyeri	6	394,293	284,042	18.52	14-Feb-11
A/Kenya/CDC-Nyeri/039/2011_22-Feb-2011	EPI_ISL_428937	Nyeri	6	1,254,603	455,950	29.24	22-Feb-11
A/Kenya/CDC-Nyeri/040/2011_24-Feb-2011	EPI_ISL_428938	Nyeri	6	408,761	387,076	23.57	24-Feb-11
A/Kenya/CDC-Nyeri/041/2011_18-Apr-2011	EPI_ISL_428963	Nyeri	6	457,069	78,486	25.8	18-Apr-11
A/Kenya/CDC-Nyeri/042/2011_06-Jul-2011	EPI_ISL_428964	Nyeri	6	370,555	293,193	24.66	06-Jul-11
A/Kenya/CDC-Nyeri/044/2011_13-Jul-2011	EPI_ISL_428965	Nyeri	6	306,626	260,677	18.88	13-Jul-11
A/Kenya/CDC-Nyeri/045/2011_20-Jul-2011	EPI_ISL_428966	Nyeri	6	364,916	223,390	20.98	20-Jul-11
A/Kenya/CDC-Nyeri/046/2011_22-Jul-2011	EPI_ISL_428968	Nyeri	6	343,206	41,227	25.3	22-Jul-11
A/Kenya/CDC-Nyeri/047/2011_29-Jul-2011	EPI_ISL_428967	Nyeri	6	340,383	66,795	22.8	29-Jul-11
A/Kenya/CDC-Nyeri/062/2014_28-Apr-2014	EPI_ISL_428970	Nyeri	6B	974,971	798,039	25.09	28-Apr-14
A/Kenya/CDC-Nyeri/065/2014_03-Jun-2014	EPI_ISL_428971	Nyeri	6B	382,530	365,663	28.99	03-Jun-14
A/Kenya/CDC-Nyeri/066/2014_10-Jun-2014	EPI_ISL_428972	Nyeri	6B	451,731	160,030	27.22	10-Jun-14
A/Kenya/CDC-Nyeri/067/2014_18-Jun-2014	EPI_ISL_428973	Nyeri	6B	448,798	421,859	27.82	18-Jun-14
A/Kenya/CDC-Nyeri/071/2014_02-Jul-2014	EPI_ISL_428974	Nyeri	6B	421,534	51,542	30.4	02-Jul-14
A/Kenya/CDC-Nyeri/072/2014_02-Jul-2014	EPI_ISL_428975	Nyeri	6B	441,520	130,825	33.2	02-Jul-14
A/Kenya/CDC-Nyeri/074/2014_07-Jul-2014	EPI_ISL_428976	Nyeri	6B	361,100	108,207	24.28	07-Jul-14
A/Kenya/CDC-Nyeri/075/2014_06-Aug-2014	EPI_ISL_428977	Nyeri	6B	472,649	51,420	31.55	06-Aug-14
A/Kenya/CDC-Nyeri/077/2015_22-Jul-2015	EPI_ISL_428978	Nyeri	6B	487,801	450,015	35.09	22-Jul-15
A/Kenya/CDC-Nyeri/078/2015_27-Jul-2015	EPI_ISL_428979	Nyeri	6B	458,049	354,660	25.9	27-Jul-15

A/Kenya/CDC-Nyeri/080/2015_12-Aug-2015	EPI_ISL_428980	Nyeri	6B.1	469,748	113,947	23.4	12-Aug-15
A/Kenya/CDC-Nyeri/081/2015_12-Aug-2015	EPI_ISL_428981	Nyeri	6B	512,380	476,909	26.7	12-Aug-15
A/Kenya/CDC-Nyeri/082/2016_04-Jan-2016	EPI_ISL_428982	Nyeri	6B	386,698	367,396	31	04-Jan-16
A/Kenya/CDC-Nyeri/083/2016_23-Aug-2016	EPI_ISL_428983	Nyeri	6B	364,278	281,251	23.9	23-Aug-16
A/Kenya/CDC-Nyeri/084/2016_30-Aug-2016	EPI_ISL_428984	Nyeri	6B.1	357,839	197,733	23	30-Aug-16
A/Kenya/CDC-Nyeri/001/2018_28-May-2018	EPI_ISL_428985	Nyeri	6B.1A	359,216	267,976	24.88	28-May-18
A/Kenya/CDC-Nyeri/002/2018_25-Jun-2018	EPI_ISL_428986	Nyeri	6B.1A	374,328	283,519	26.91	25-Jun-18
A/Kenya/CDC-Nyeri/004/2018_09-Apr-2018	EPI_ISL_428987	Nyeri	6B.1A	445,883	307,349	24.4	09-Apr-18
A/Kenya/CDC-Nyeri/005/2018_18-Jun-2018	EPI_ISL_428988	Nyeri	6B.1A	337,973	250,491	22.91	18-Jun-18
A/Kenya/CDC-Nyeri/008/2018_11-Jun-2018	EPI_ISL_428989	Nyeri	6B.1A	250,712	192,876	23.62	11-Jun-18
A/Kenya/CDC-Siaya/001/2009_16-Nov-2009	EPI_ISL_429224	Siaya	7	482,013	117,848	30.18	16-Nov-09
A/Kenya/CDC-Siaya/002/2009_07-Oct-2009	EPI_ISL_429225	Siaya	7	580,801	475,818	28.09	07-Oct-09
A/Kenya/CDC-Siaya/004/2009_14-Oct-2009	EPI_ISL_429237	Siaya	7	612,685	23,782	28.28	14-Oct-09
A/Kenya/CDC-Siaya/006/2009_19-Oct-2009	EPI_ISL_429238	Siaya	7	702,636	18,810	30.1	19-Oct-09
A/Kenya/CDC-Siaya/007/2009_19-Oct-2009	EPI_ISL_429240	Siaya	7	344,347	279,618	21.41	19-Oct-09
A/Kenya/CDC-Siaya/008/2009_18-Oct-2009	EPI_ISL_429241	Siaya	7	488,879	15,495	25.36	18-Oct-09
A/Kenya/CDC-Siaya/009/2009_21-Oct-2009	EPI_ISL_429242	Siaya	7	482,326	274,009	28.88	21-Oct-09
A/Kenya/CDC-Siaya/011/2009_10-Sep-2009	EPI_ISL_429243	Siaya	7	548,392	502,827	22.15	10-Sep-09
A/Kenya/CDC-Siaya/012/2009_29-Sep-2009	EPI_ISL_429244	Siaya	7	468,523	272,265	25.76	29-Sep-09
A/Kenya/CDC-Siaya/013/2009_30-Sep-2009	EPI_ISL_429245	Siaya	7	451,523	243,549	30.02	30-Sep-09
A/Kenya/CDC-Siaya/015/2009_16-Nov-2009	EPI_ISL_429246	Siaya	7	511,902	154,018	28.5	16-Nov-09
A/Kenya/CDC-Siaya/018/2010_19-Feb-2010	EPI_ISL_429247	Siaya	7	561,527	282,027	29.21	19-Feb-10
A/Kenya/CDC-Siaya/019/2010_05-Nov-2010	EPI_ISL_429248	Siaya	6	586,730	131,485	27.27	05-Nov-10
A/Kenya/CDC-Siaya/020/2010_16-Nov-2010	EPI_ISL_429252	Siaya	6	684,756	626,658	22.09	16-Nov-10
A/Kenya/CDC-Siaya/021/2010_18-Nov-2010	EPI_ISL_429253	Siaya	6	207,735	160,610	21.82	18-Nov-10
A/Kenya/CDC-Siaya/022/2010_24-Nov-2010	EPI_ISL_429260	Siaya	6	566,375	171,772	23.72	24-Nov-10
A/Kenya/CDC-Siaya/023/2010_28-Nov-2010	EPI_ISL_429261	Siaya	6	427,217	283,526	23.65	28-Nov-10
A/Kenya/CDC-Siaya/025/2011_25-Jan-2011	EPI_ISL_429319	Siaya	6	457,490	438,053	19.54	25-Jan-11

A/Kenya/CDC-Siaya/026/2011_08-Feb-2011	EPI_ISL_429591	Siaya	6	386,638	110,628	26.07	08-Feb-11
A/Kenya/CDC-Siaya/027/2011_10-Feb-2011	EPI_ISL_429592	Siaya	6	759,471	31,734	29.43	10-Feb-11
A/Kenya/CDC-Siaya/028/2011_16-Feb-2011	EPI_ISL_429593	Siaya	6	780,143	299,617	23.09	16-Feb-11
A/Kenya/CDC-Siaya/029/2011_15-Feb-2011	EPI_ISL_429594	Siaya	6	732,596	335,112	26.61	15-Feb-11
A/Kenya/CDC-Siaya/030/2011_16-Feb-2011	EPI_ISL_429595	Siaya	6	501,579	9,451	29.74	16-Feb-11
A/Kenya/CDC-Siaya/032/2011_21-Feb-2011	EPI_ISL_429596	Siaya	6	413,310	114,548	26.8	21-Feb-11
A/Kenya/CDC-Siaya/033/2011_21-Feb-2011	EPI_ISL_429660	Siaya	6	357,111	14,706	28.46	21-Feb-11
A/Kenya/CDC-Siaya/035/2011_28-Feb-2011	EPI_ISL_429661	Siaya	6	482,543	48,385	31.07	28-Feb-11
A/Kenya/CDC-Siaya/036/2011_01-Mar-2011	EPI_ISL_429662	Siaya	6	469,058	157,101	28.08	01-Mar-11
A/Kenya/CDC-Siaya/037/2011_28-Feb-2011	EPI_ISL_429704	Siaya	6	435,508	263,340	22.93	28-Feb-11
A/Kenya/CDC-Siaya/038/2011_07-Mar-2011	EPI_ISL_429801	Siaya	6	445,075	394,407	21.09	07-Mar-11
A/Kenya/CDC-Siaya/039/2011_10-Mar-2011	EPI_ISL_429804	Siaya	6	1,318,841	1,248,668	22.13	10-Mar-11
A/Kenya/CDC-Siaya/040/2011_11-Mar-2011	EPI_ISL_429823	Siaya	6	459,167	399,434	26.13	11-Mar-11
A/Kenya/CDC-Siaya/041/2011_11-Mar-2011	EPI_ISL_429824	Siaya	6	503,606	378,273	21.28	11-Mar-11
A/Kenya/CDC-Siaya/042/2011_11-Mar-2011	EPI_ISL_429825	Siaya	6	413,020	267,216	34.62	11-Mar-11
A/Kenya/CDC-Siaya/043/2011_13-Apr-2011	EPI_ISL_429826	Siaya	7	501,060	140,456	26.47	13-Apr-11
A/Kenya/CDC-Siaya/044/2011_07-Nov-2011	EPI_ISL_429827	Siaya	6	875,890	815,001	17.44	07-Nov-11
A/Kenya/CDC-Siaya/045/2011_10-Nov-2011	EPI_ISL_429828	Siaya	6	420,488	395,777	22.81	10-Nov-11
A/Kenya/CDC-Siaya/047/2013_04-Feb-2013	EPI_ISL_429829	Siaya	6C	1,276,097	1,214,482	25.38	04-Feb-13
A/Kenya/CDC-Siaya/048/2013_07-Feb-2013	EPI_ISL_429830	Siaya	6C	774,380	745,384	21.43	07-Feb-13
A/Kenya/CDC-Siaya/049/2013_27-Feb-2013	EPI_ISL_429832	Siaya	6C	751,855	638,547	21.07	27-Feb-13
A/Kenya/CDC-Siaya/050/2011_14-Mar-2011	EPI_ISL_429833	Siaya	6	307,921	151,863	29.67	14-Mar-11
A/Kenya/CDC-Siaya/051/2011_14-Mar-2011	EPI_ISL_429834	Siaya	6	393,999	338,043	23.28	14-Mar-11
A/Kenya/CDC-Siaya/052/2011_16-Mar-2011	EPI_ISL_429835	Siaya	6	343,386	331,491	33.41	16-Mar-11
A/Kenya/CDC-Siaya/056/2013_11-Feb-2013	EPI_ISL_429836	Siaya	6C	446,486	231,950	31.72	11-Feb-13

7.2.2 Influenza A(H3N2) Virus, Kilifi, Kenya 2015-2016

Sample Name	GISAID Accession	Health Facility	Clade	No. of Reads	IAV Reads	PCR Ct	Collection Date
A/Kilifi/051/2015_15-Dec-2015	EPI_ISL_393711	Chasimba	3C.2a	133,717	23,232	33.36	15-Dec-15
A/Kilifi/052/2015_15-Dec-2015	EPI_ISL_393712	Chasimba	3C.2a	136,794	131,291	24.08	15-Dec-15
A/Kilifi/053/2015_15-Dec-2015	EPI_ISL_393713	Chasimba	3C.2a	255,309	240,444	27.42	15-Dec-15
A/Kilifi/054/2015_15-Dec-2015	EPI_ISL_393714	Chasimba	3C.2a	132,165	85,125	25.67	15-Dec-15
A/Kilifi/055/2016_16-Nov-2016	EPI_ISL_393715	Chasimba	3C.2a1b	99,374	91,037	23.23	16-Nov-16
A/Kilifi/056/2016_21-Jun-2016	EPI_ISL_393716	Chasimba	3C.2a1b	324,996	282,265	22.77	21-Jun-16
A/Kilifi/057/2016_23-Nov-2016	EPI_ISL_393717	Chasimba	3C.2a1b	186,969	162,732	26.98	23-Nov-16
A/Kilifi/059/2015_14-Dec-2015	EPI_ISL_393719	Jaribuni	3C.2a	83,859	80,232	32.86	14-Dec-15
A/Kilifi/060/2015_18-Dec-2015	EPI_ISL_393720	Jaribuni	3C.2a	59,150	56,250	25.23	18-Dec-15
A/Kilifi/061/2015_21-Dec-2015	EPI_ISL_393721	Jaribuni	3C.2a	112,024	48,180	32.39	21-Dec-15
A/Kilifi/062/2016_20-Jan-2016	EPI_ISL_393722	Jaribuni	3C.2a	154,372	144,075	25.37	20-Jan-16
A/Kilifi/068/2015_15-Dec-2015	EPI_ISL_393725	Junju	3C.2a	145,454	131,035	30.71	15-Dec-15
A/Kilifi/069/2016_18-Jan-2016	EPI_ISL_393726	Junju	3C.2a	129,423	105,053	29.04	18-Jan-16
A/Kilifi/070/2016_27-Jan-2016	EPI_ISL_393727	Junju	3C.2a	213,306	187,913	22.64	27-Jan-16
A/Kilifi/071/2016_04-Feb-2016	EPI_ISL_393728	Junju	3C.2a	153,652	132,279	26.43	04-Feb-16
A/Kilifi/072/2016_04-Feb-2016	EPI_ISL_393729	Junju	3C.2a	156,725	78,748	31.49	04-Feb-16
A/Kilifi/074/2015_15-Dec-2015	EPI_ISL_393730	Matsangoni	3C.2a	205,535	177,326	28.31	15-Dec-15
A/Kilifi/075/2015_15-Dec-2015	EPI_ISL_393731	Matsangoni	3C.2a	109,504	96,193	24.14	15-Dec-15
A/Kilifi/076/2016_14-Jan-2016	EPI_ISL_393732	Matsangoni	3C.2a	50,268	49,003	24.87	14-Jan-16
A/Kilifi/077/2016_14-Jan-2016	EPI_ISL_393733	Matsangoni	3C.2a	123,762	111,809	29	14-Jan-16
A/Kilifi/078/2016_21-Jan-2016	EPI_ISL_393734	Matsangoni	3C.2a	164,429	72,862	27.58	21-Jan-16
A/Kilifi/079/2016_21-Jan-2016	EPI_ISL_393735	Matsangoni	3C.2a	307,159	278,358	25.39	21-Jan-16

A/Kilifi/080/2016_26-Jan-2016	EPI_ISL_393736	Matsangoni	3C.2a	189,597	114,700	25.58	26-Jan-16
A/Kilifi/081/2016_18-Feb-2016	EPI_ISL_393737	Matsangoni	3C.2a	146,316	49,319	30.25	18-Feb-16
A/Kilifi/082/2016_18-Feb-2016	EPI_ISL_393738	Matsangoni	3C.2a	200,899	173,947	26.87	18-Feb-16
A/Kilifi/083/2016_18-Feb-2016	EPI_ISL_393739	Matsangoni	3C.2a	190,298	152,627	29.41	18-Feb-16
A/Kilifi/084/2016_17-Nov-2016	EPI_ISL_393740	Matsangoni	3C.2a1b	234,407	210,230	25.88	17-Nov-16
A/Kilifi/085/2016_17-Nov-2016	EPI_ISL_393741	Matsangoni	3C.2a1b	158,074	61,337	33.13	17-Nov-16
A/Kilifi/086/2016_24-Nov-2016	EPI_ISL_393742	Matsangoni	3C.2a1b	260,065	184,316	27.81	24-Nov-16
A/Kilifi/087/2016_24-Nov-2016	EPI_ISL_393743	Matsangoni	3C.2a1b	227,566	107,856	27.08	24-Nov-16
A/Kilifi/088/2016_24-Nov-2016	EPI_ISL_393744	Matsangoni	3C.2a1b	271,903	240,451	25.11	24-Nov-16
A/Kilifi/089/2016_29-Nov-2016	EPI_ISL_393745	Matsangoni	3C.2a1b	279,517	268,860	25.18	29-Nov-16
A/Kilifi/090/2016_29-Nov-2016	EPI_ISL_393746	Matsangoni	3C.2a1b	208,946	159,098	28.24	29-Nov-16
A/Kilifi/092/2015_14-Dec-2015	EPI_ISL_393748	Mavueni	3C.2a	133,596	115,661	24.51	14-Dec-15
A/Kilifi/093/2016_16-Nov-2016	EPI_ISL_393749	Mavueni	3C.2a1b	197,226	183,062	25.37	16-Nov-16
A/Kilifi/094/2016_16-Nov-2016	EPI_ISL_393750	Mavueni	3C.2a1b	258,198	241,015	28.56	16-Nov-16
A/Kilifi/096/2016_23-Nov-2016	EPI_ISL_393751	Mavueni	3C.2a3	216,940	196,678	24.34	23-Nov-16
A/Kilifi/097/2016_28-Nov-2016	EPI_ISL_393752	Mavueni	3C.2a1b	427,356	403,263	25.42	28-Nov-16
A/Kilifi/099/2015_15-Dec-2015	EPI_ISL_393936	Mtondia	3C.2a	213,672	97,215	33.89	15-Dec-15
A/Kilifi/100/2015_14-Dec-2015	EPI_ISL_393937	Mtondia	3C.2a	247,285	57,649	30.87	14-Dec-15
A/Kilifi/101/2015_15-Dec-2015	EPI_ISL_393938	Mtondia	3C.2a	264,430	216,668	27.45	15-Dec-15
A/Kilifi/102/2015_17-Dec-2015	EPI_ISL_393939	Mtondia	3C.2a	381,087	369,662	21.43	17-Dec-15
A/Kilifi/103/2016_11-Jan-2016	EPI_ISL_393940	Mtondia	3C.2a	236,363	9,514	27.77	11-Jan-16
A/Kilifi/104/2016_03-Feb-2016	EPI_ISL_393941	Mtondia	3C.2a	266,812	205,626	22.8	03-Feb-16
A/Kilifi/105/2016_01-Mar-2016	EPI_ISL_393942	Mtondia	3C.2a	268,033	235,530	34.38	01-Mar-16
A/Kilifi/106/2016_14-Nov-2016	EPI_ISL_393943	Mtondia	3C.2a1b	284,652	159,170	26.63	14-Nov-16
A/Kilifi/107/2016_01-Dec-2016	EPI_ISL_393944	Mtondia	3C.2a1b	289,721	280,873	22.37	01-Dec-16
A/Kilifi/108/2016_02-Dec-2016	EPI_ISL_393945	Mtondia	3C.2a1b	206,719	180,831	30.18	02-Dec-16

A/Kilifi/109/2016_06-Jun-2016	EPI_ISL_393946	Ngerenya	3C.2a2	190,576	15,729	31.02	06-Jun-16
A/Kilifi/110/2016_06-Jun-2016	EPI_ISL_393949	Ngerenya	3C.2a2	225,418	192,427	26.1	06-Jun-16
A/Kilifi/111/2016_14-Nov-2016	EPI_ISL_393951	Ngerenya	3C.2a1b	196,416	154,224	26.35	14-Nov-16
A/Kilifi/112/2016_29-Nov-2016	EPI_ISL_393952	Ngerenya	3C.2a1b	200,841	192,724	23.9	29-Nov-16
A/Kilifi/114/2015_14-Dec-2015	EPI_ISL_393955	Pingilikani	3C.2a	175,812	171,555	26.2	14-Dec-15
A/Kilifi/115/2016_27-Jan-2016	EPI_ISL_393956	Pingilikani	3C.2a	225,510	182,056	26.08	27-Jan-16
A/Kilifi/116/2016_18-May-2016	EPI_ISL_393960	Pingilikani	3C.2a2	275,921	169,739	24.99	18-May-16
A/Kilifi/117/2015_15-Dec-2015	EPI_ISL_393963	Sokoke	3C.2a	181,937	166,814	26.3	15-Dec-15
A/Kilifi/118/2016_01-Dec-2016	EPI_ISL_393965	Sokoke	3C.2a1b	231,390	214,827	25.51	01-Dec-16
A/Kilifi/119/2016_05-Dec-2016	EPI_ISL_393966	Sokoke	3C.2a1b	203,938	198,183	21.41	05-Dec-16

7.2.3 Influenza A(H1N1)pdm09 and A(H3N2) Viruses, PERCH-Africa, 2011-2013

Sample	GISAID Accession	Country	Subtype	Total Reads	IAV Reads	PCR Ct	Collection Date	PERCH Status
A/Gambia-PERCH/003/2011_14-Nov-2011	EPI_ISL_509524	The Gambia	H3N2	682,758	356,562	30.93	14-Nov-11	Control
A/Gambia-PERCH/005/2013_17-Sep-2013	EPI_ISL_509525	The Gambia	H3N2	758,836	670,471	30.12	17-Sep-13	Control
A/Gambia-PERCH/006/2012_12-Nov-2012	EPI_ISL_509526	The Gambia	H3N2	428,896	282,176	29.78	12-Nov-12	Case
A/Gambia-PERCH/007/2012_13-Nov-2012	EPI_ISL_509564	The Gambia	H3N2	593,590	425,081	29.7	13-Nov-12	Control
A/Gambia-PERCH/008/2012_08-Nov-2012	EPI_ISL_509565	The Gambia	H3N2	350,776	197,205	29.69	08-Nov-12	Control
A/Gambia-PERCH/009/2012_30-Oct-2012	EPI_ISL_509566	The Gambia	H3N2	458,082	165,944	28.81	30-Oct-12	Case
A/Gambia-PERCH/010/2012_19-Nov-2012	EPI_ISL_509655	The Gambia	H3N2	710,322	493,533	28.79	19-Nov-12	Control
A/Gambia-PERCH/011/2012_30-Oct-2012	EPI_ISL_509656	The Gambia	H3N2	899,338	621,077	28.12	30-Oct-12	Case
A/Gambia-PERCH/012/2012_02-Nov-2012	EPI_ISL_509657	The Gambia	H3N2	687,144	448,606	28.08	02-Nov-12	Case
A/Gambia-PERCH/013/2012_17-Nov-2012	EPI_ISL_509658	The Gambia	H3N2	1,043,410	807,421	27.8	17-Nov-12	Case
A/Gambia-PERCH/014/2012_29-Oct-2012	EPI_ISL_509659	The Gambia	H3N2	695,670	502,447	27.44	29-Oct-12	Case
A/Gambia-PERCH/015/2012_27-Oct-2012	EPI_ISL_509660	The Gambia	H3N2	720,224	516,616	26.49	27-Oct-12	Case
A/Gambia-PERCH/016/2012_12-Nov-2012	EPI_ISL_509661	The Gambia	H3N2	996,836	729,878	26.15	12-Nov-12	Case
A/Gambia-PERCH/017/2013_30-Sep-2013	EPI_ISL_509669	The Gambia	H3N2	609,804	392,815	25.91	30-Sep-13	Case
A/Gambia-PERCH/022/2012_08-Nov-2012	EPI_ISL_509687	The Gambia	H3N2	350,792	227,309	31.81	08-Nov-12	Case
A/Kenya-PERCH/003/2012_21-Nov-2012	EPI_ISL_510040	Kenya	H3N2	323,438	315,918	23	21-Nov-12	Control
A/Kenya-PERCH/005/2012_24-Oct-2012	EPI_ISL_510041	Kenya	H3N2	229,734	209,397	26	24-Oct-12	Case
A/Kenya-PERCH/006/2012_07-Nov-2012	EPI_ISL_510042	Kenya	H3N2	240,823	233,526	27	07-Nov-12	Case
A/Kenya-PERCH/007/2012_08-Nov-2012	EPI_ISL_510043	Kenya	H3N2	457,988	432,062	26	08-Nov-12	Case
A/Kenya-PERCH/008/2011_25-Nov-2011	EPI_ISL_510078	Kenya	H3N2	500,585	205,112	32	25-Nov-11	Case
A/Kenya-PERCH/010/2011_17-Dec-2011	EPI_ISL_510079	Kenya	H3N2	351,879	72,599	31	17-Dec-11	Case
A/Kenya-PERCH/013/2012_29-Nov-2012	EPI_ISL_510080	Kenya	H3N2	247,310	236,163	29	29-Nov-12	Case
A/Kenya-PERCH/014/2012_27-Nov-2012	EPI_ISL_510102	Kenya	H3N2	237,118	224,545	27	27-Nov-12	Case

A/Mali-PERCH/003/2013_09-Oct-2013	EPI_ISL_510152	Mali	H3N2	316,493	295,494	34.82	09-Oct-13	Control
A/Mali-PERCH/006/2012_07-Sep-2012	EPI_ISL_510153	Mali	H3N2	305,618	29,586	31.2	07-Sep-12	Case
A/Mali-PERCH/008/2012_10-Apr-2012	EPI_ISL_510154	Mali	H3N2	1,551,650	1,143,322	30.36	10-Apr-12	Control
A/Mali-PERCH/014/2013_07-Oct-2013	EPI_ISL_510155	Mali	H3N2	297,560	37,275	28.87	07-Oct-13	Control
A/Mali-PERCH/015/2012_10-Apr-2012	EPI_ISL_510156	Mali	H3N2	386,550	1,971	28.11	10-Apr-12	Case
A/Mali-PERCH/017/2012_13-Mar-2012	EPI_ISL_510157	Mali	H3N2	195,754	6,141	26.8	13-Mar-12	Case
A/Mali-PERCH/019/2013_09-Sep-2013	EPI_ISL_510158	Mali	H3N2	133,898	81,069	25.31	09-Sep-13	Control
A/Mali-PERCH/021/2013_02-Oct-2013	EPI_ISL_510159	Mali	H3N2	785,736	421,915	25.11	02-Oct-13	Control
A/South-Africa-PERCH/002/2011_03-Sep-2011	EPI_ISL_509025	South Africa	H3N2	959,024	244,566	27.85	03-Sep-11	Case
A/South-Africa-PERCH/003/2011_11-Sep-2011	EPI_ISL_509027	South Africa	H3N2	238,632	54,824	27.1	11-Sep-11	Case
A/South-Africa-PERCH/004/2011_20-Sep-2011	EPI_ISL_509030	South Africa	H3N2	348,410	18,801	30.99	20-Sep-11	Control
A/South-Africa-PERCH/005/2011_03-Oct-2011	EPI_ISL_509032	South Africa	H3N2	469,614	254,355	25.73	03-Oct-11	Case
A/South-Africa-PERCH/006/2012_11-Jun-2012	EPI_ISL_509034	South Africa	H3N2	272,092	179,892	22.2	11-Jun-12	Case
A/South-Africa-PERCH/007/2012_12-Jun-2012	EPI_ISL_509036	South Africa	H3N2	201,926	100,539	27.73	12-Jun-12	Case
A/South-Africa-PERCH/008/2012_20-Jun-2012	EPI_ISL_509039	South Africa	H3N2	273,130	98,606	25.59	20-Jun-12	Case
A/South-Africa-PERCH/009/2012_02-Jul-2012	EPI_ISL_509042	South Africa	H3N2	362,708	223,310	21.63	02-Jul-12	Case
A/South-Africa-PERCH/010/2012_05-Jul-2012	EPI_ISL_509043	South Africa	H3N2	173,768	93,113	22.44	05-Jul-12	Case
A/South-Africa-PERCH/011/2012_11-Jul-2012	EPI_ISL_509044	South Africa	H3N2	545,962	253,471	27.32	11-Jul-12	Case
A/South-Africa-PERCH/012/2012_03-Aug-2012	EPI_ISL_509045	South Africa	H3N2	581,442	301,043	27.14	03-Aug-12	Case
A/South-Africa-PERCH/017/2013_18-Jun-2013	EPI_ISL_509046	South Africa	H3N2	269,620	2,921	31.21	18-Jun-13	Control
A/South-Africa-PERCH/025/2013_27-Jun-2013	EPI_ISL_509047	South Africa	H3N2	106,046	65,947	24.63	27-Jun-13	Case
A/South-Africa-PERCH/026/2013_01-Jul-2013	EPI_ISL_509048	South Africa	H3N2	391,390	93,015	22.69	01-Jul-13	Case
A/South-Africa-PERCH/027/2013_01-Jul-2013	EPI_ISL_509049	South Africa	H3N2	54,990	3,858	32.79	01-Jul-13	Case
A/South-Africa-PERCH/028/2013_01-Jul-2013	EPI_ISL_509050	South Africa	H3N2	711,118	371,854	26.03	01-Jul-13	Case
A/South-Africa-PERCH/029/2013_04-Jul-2013	EPI_ISL_509052	South Africa	H3N2	225,492	155,996	22.92	04-Jul-13	Case
A/South-Africa-PERCH/030/2013_25-Jun-2013	EPI_ISL_509053	South Africa	H3N2	868,844	553,942	23.62	25-Jun-13	Control
A/South-Africa-PERCH/035/2013_04-Jul-2013	EPI_ISL_509054	South Africa	H3N2	748,732	508,991	22.41	04-Jul-13	Case

A/South-Africa-PERCH/037/2013_22-Jul-2013	EPI_ISL_509055	South Africa	H3N2	92,174	58,840	22.37	22-Jul-13	Case
A/South-Africa-PERCH/038/2013_30-Jul-2013	EPI_ISL_509056	South Africa	H3N2	150,260	113,412	24.17	30-Jul-13	Control
A/South-Africa-PERCH/039/2013_14-Aug-2013	EPI_ISL_509057	South Africa	H3N2	100,094	68,435	21.68	14-Aug-13	Case
A/South-Africa-PERCH/040/2013_27-Aug-2013	EPI_ISL_509058	South Africa	H3N2	214,888	96,121	25.32	27-Aug-13	Case
A/Zambia-PERCH/003/2013_26-Sep-2013	EPI_ISL_509396	Zambia	H3N2	380,352	40,589	33.42	26-Sep-13	Case
A/Zambia-PERCH/004/2012_21-Mar-2012	EPI_ISL_509397	Zambia	H3N2	734,200	244,685	33.31	21-Mar-12	Control
A/Zambia-PERCH/005/2012_22-Feb-2012	EPI_ISL_509398	Zambia	H3N2	286,680	193,538	27.48	22-Feb-12	Control
A/Zambia-PERCH/007/2012_26-Feb-2012	EPI_ISL_509399	Zambia	H3N2	177,154	123,155	25.51	26-Feb-12	Case
A/Zambia-PERCH/008/2012_16-Mar-2012	EPI_ISL_509400	Zambia	H3N2	493,900	268,444	30.48	16-Mar-12	Case
A/Zambia-PERCH/009/2012_05-Jul-2012	EPI_ISL_509401	Zambia	H3N2	234,868	163,943	27.9	05-Jul-12	Case
A/Zambia-PERCH/010/2012_24-Aug-2012	EPI_ISL_509402	Zambia	H3N2	455,170	306,493	31.22	24-Aug-12	Case
A/Zambia-PERCH/012/2012_28-Sep-2012	EPI_ISL_509404	Zambia	H3N2	306,297	296,336	28.22	28-Sep-12	Case
A/Zambia-PERCH/014/2012_19-Oct-2012	EPI_ISL_509405	Zambia	H3N2	561,300	497,325	31.94	19-Oct-12	Case
A/Zambia-PERCH/020/2013_07-Aug-2013	EPI_ISL_509406	Zambia	H3N2	427,365	410,850	30.82	07-Aug-13	Case
A/Zambia-PERCH/021/2013_18-Aug-2013	EPI_ISL_509407	Zambia	H3N2	578,943	557,469	25.94	18-Aug-13	Case
A/Zambia-PERCH/022/2013_22-Aug-2013	EPI_ISL_509408	Zambia	H3N2	711,181	711,181	26.61	22-Aug-13	Control
A/Zambia-PERCH/024/2013_12-Sep-2013	EPI_ISL_509409	Zambia	H3N2	326,469	320,918	28.33	12-Sep-13	Case
A/Zambia-PERCH/025/2013_12-Sep-2013	EPI_ISL_509410	Zambia	H3N2	297,108	285,315	26.97	12-Sep-13	Case
A/Zambia-PERCH/026/2013_16-Sep-2013	EPI_ISL_509411	Zambia	H3N2	343,942	16,649	28.95	16-Sep-13	Case
A/Gambia-PERCH/002/2013_25-Feb-2013	EPI_ISL_511774	The Gambia	H1N1pdm09	602,064	87,721	31.83	25-Feb-13	Case
A/Gambia-PERCH/004/2013_18-Oct-2013	EPI_ISL_511775	The Gambia	H1N1pdm09	749,190	479,620	30.42	18-Oct-13	Case
A/Gambia-PERCH/018/2013_01-Oct-2013	EPI_ISL_511776	The Gambia	H1N1pdm09	393,134	121,256	25.36	01-Oct-13	Case
A/Kenya-PERCH/004/2013_10-May-2013	EPI_ISL_511777	Kenya	H1N1pdm09	312,528	269,798	23	10-May-13	Case
A/Kenya-PERCH/012/2013_25-Sep-2013	EPI_ISL_511778	Kenya	H1N1pdm09	231,385	123,447	24	25-Sep-13	Case
A/Mali-PERCH/004/2013_12-Sep-2013	EPI_ISL_511779	Mali	H1N1pdm09	417,952	169,938	33.42	12-Sep-13	Control
A/Mali-PERCH/005/2013_02-Oct-2013	EPI_ISL_511780	Mali	H1N1pdm09	623,968	297,786	33.38	02-Oct-13	Control
A/Mali-PERCH/007/2012_17-Mar-2012	EPI_ISL_511781	Mali	H1N1pdm09	216,146	54,860	30.94	17-Mar-12	Case

A/Mali-PERCH/009/2012_21-Aug-2012	EPI_ISL_511782	Mali	H1N1pdm09	651,814	174,750	29.78	21-Aug-12	Case
A/Mali-PERCH/010/2013_19-Mar-2013	EPI_ISL_511783	Mali	H1N1pdm09	682,752	197,581	29.73	19-Mar-13	Case
A/Mali-PERCH/011/2012_24-Sep-2012	EPI_ISL_511784	Mali	H1N1pdm09	385,440	158,458	29.23	24-Sep-12	Case
A/Mali-PERCH/012/2013_27-May-2013	EPI_ISL_511785	Mali	H1N1pdm09	400,014	164,297	29.15	27-May-13	Case
A/Mali-PERCH/013/2013_08-Apr-2013	EPI_ISL_511786	Mali	H1N1pdm09	571,292	175,534	29.03	08-Apr-13	Case
A/Mali-PERCH/020/2013_13-Feb-2013	EPI_ISL_511787	Mali	H1N1pdm09	202,926	129,843	25.12	13-Feb-13	Case
A/Mali-PERCH/022/2013_16-Sep-2013	EPI_ISL_511788	Mali	H1N1pdm09	270,648	14,402	23.93	16-Sep-13	Case
A/South-Africa-PERCH/013/2013_17-Mar-2013	EPI_ISL_511789	South Africa	H1N1pdm09	640,774	449,639	23.19	17-Mar-13	Case
A/South-Africa-PERCH/014/2013_27-May-2013	EPI_ISL_511790	South Africa	H1N1pdm09	407,696	123,393	25.14	27-May-13	Case
A/South-Africa-PERCH/015/2013_11-Jun-2013	EPI_ISL_511791	South Africa	H1N1pdm09	722,238	305,685	26.72	11-Jun-13	Case
A/South-Africa-PERCH/016/2013_11-Jun-2013	EPI_ISL_511792	South Africa	H1N1pdm09	211,520	45,473	26.88	11-Jun-13	Case
A/South-Africa-PERCH/019/2013_20-Jun-2013	EPI_ISL_511793	South Africa	H1N1pdm09	257,618	132,330	29.38	20-Jun-13	Control
A/South-Africa-PERCH/021/2013_13-Jun-2013	EPI_ISL_511794	South Africa	H1N1pdm09	442,502	311,055	23.46	13-Jun-13	Case
A/South-Africa-PERCH/022/2013_24-Jun-2013	EPI_ISL_511795	South Africa	H1N1pdm09	181,330	27,838	32.15	24-Jun-13	Case
A/South-Africa-PERCH/023/2013_25-Jun-2013	EPI_ISL_511796	South Africa	H1N1pdm09	302,240	57,837	26.93	25-Jun-13	Case
A/South-Africa-PERCH/024/2013_27-Jun-2013	EPI_ISL_511797	South Africa	H1N1pdm09	465,958	318,425	24.82	27-Jun-13	Case
A/South-Africa-PERCH/033/2013_05-Jul-2013	EPI_ISL_511798	South Africa	H1N1pdm09	345,186	237,447	20.76	05-Jul-13	Control
A/South-Africa-PERCH/034/2013_04-Jul-2013	EPI_ISL_511799	South Africa	H1N1pdm09	468,878	33,023	23.16	04-Jul-13	Case
A/Zambia-PERCH/002/2013_08-Feb-2013	EPI_ISL_511800	Zambia	H1N1pdm09	390,392	87,520	34.18	08-Feb-13	Case
A/Zambia-PERCH/016/2013_07-Feb-2013	EPI_ISL_511801	Zambia	H1N1pdm09	344,752	243,721	26.22	07-Feb-13	Control
A/Zambia-PERCH/017/2013_12-Feb-2013	EPI_ISL_511802	Zambia	H1N1pdm09	671,640	282,467	30.56	12-Feb-13	Control
A/Zambia-PERCH/018/2013_18-Feb-2013	EPI_ISL_511803	Zambia	H1N1pdm09	479,052	363,370	28.39	18-Feb-13	Case
A/Zambia-PERCH/019/2013_21-Feb-2013	EPI_ISL_511804	Zambia	H1N1pdm09	592,623	252,294	30.5	21-Feb-13	Case

7.3 Genome Details for Global Datasets from GISAID Database

7.3.1 Global Influenza A(H1N1)pdm09 Virus Genome Details, 2009-2018

Isolate Name	GISAID Accession	Continent	Country
A/Antananarivo/1089/2016	EPI_ISL_230471	Africa	Madagascar
A/Antsirabe/4350/2015	EPI_ISL_207922	Africa	Madagascar
A/Antsirabe/5599/2016	EPI_ISL_237808	Africa	Madagascar
A/Burkina Faso/042/2017	EPI_ISL_283209	Africa	Burkina Faso
A/Burkina Faso/132/2017	EPI_ISL_283222	Africa	Burkina Faso
A/Burkina Faso/133/2017	EPI_ISL_289562	Africa	Burkina Faso
A/Burkina Faso/150/2017	EPI_ISL_283231	Africa	Burkina Faso
A/Burkina Faso/154/2017	EPI_ISL_283233	Africa	Burkina Faso
A/Burkina Faso/2105/2017	EPI_ISL_283235	Africa	Burkina Faso
A/Burkina Faso/2108/2017	EPI_ISL_283237	Africa	Burkina Faso
A/Burkina Faso/583/2015	EPI_ISL_221004	Africa	Burkina Faso
A/Congo/122/2017	EPI_ISL_282765	Africa	Congo
A/Congo/1939/2015	EPI_ISL_216286	Africa	Congo
A/Congo/1941/2015	EPI_ISL_227400	Africa	Congo
A/Congo/1942/2015	EPI_ISL_218177	Africa	Congo
A/Congo/1966/2015	EPI_ISL_220999	Africa	Congo
A/Congo/1970/2015	EPI_ISL_223222	Africa	Congo
A/Congo/1973/2015	EPI_ISL_223223	Africa	Congo
A/Congo/1989/2015	EPI_ISL_223224	Africa	Congo
A/Congo/2131/2015	EPI_ISL_223229	Africa	Congo
A/Congo/2265/2015	EPI_ISL_213208	Africa	Congo
A/Congo/2275/2014	EPI_ISL_175254	Africa	Congo
A/Congo/2278/2014	EPI_ISL_175259	Africa	Congo
A/Congo/493/2017	EPI_ISL_305275	Africa	Congo
A/Congo/545/2017	EPI_ISL_305262	Africa	Congo
A/Congo/584/2017	EPI_ISL_305256	Africa	Congo
A/Congo/587/2017	EPI_ISL_305271	Africa	Congo
A/Congo/600/2017	EPI_ISL_305254	Africa	Congo
A/Congo/611/2017	EPI_ISL_305253	Africa	Congo
A/Cote D'Ivoire/1653/2017	EPI_ISL_300918	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1784/2017	EPI_ISL_300858	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1785/2017	EPI_ISL_300845	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1884/2017	EPI_ISL_305912	Africa	Cote d'Ivoire
A/Cote D'Ivoire/709/2009	EPI_ISL_34539	Africa	Cote d'Ivoire

A/Egypt/4372/2014	EPI_ISL_178484	Africa	Egypt
A/Egypt/4758/2014	EPI_ISL_178482	Africa	Egypt
A/Egypt/6194/2009	EPI_ISL_62231	Africa	Egypt
A/Ethiopia/1149/2014	EPI_ISL_172641	Africa	Ethiopia
A/Ethiopia/1396/2015	EPI_ISL_221010	Africa	Ethiopia
A/Ethiopia/1397/2015	EPI_ISL_221011	Africa	Ethiopia
A/Ethiopia/1587/2016	EPI_ISL_232686	Africa	Ethiopia
A/Ethiopia/16/2009	EPI_ISL_33576	Africa	Ethiopia
A/Ethiopia/45/2010	EPI_ISL_71367	Africa	Ethiopia
A/Ethiopia/63/2014	EPI_ISL_172648	Africa	Ethiopia
A/Ethiopia/66/2014	EPI_ISL_172640	Africa	Ethiopia
A/Kenya/101/2016	EPI_ISL_248209	Africa	Kenya
A/Kenya/104/2016	EPI_ISL_268419	Africa	Kenya
A/Kenya/106/2016	EPI_ISL_256091	Africa	Kenya
A/Kenya/108/2016	EPI_ISL_248216	Africa	Kenya
A/Kenya/109/2016	EPI_ISL_256092	Africa	Kenya
A/Kenya/126/2009	EPI_ISL_35013	Africa	Kenya
A/Kenya/196/2011	EPI_ISL_106806	Africa	Kenya
A/Kijabe/16/2010	EPI_ISL_140406	Africa	Kenya
A/Kitale/531/2009	EPI_ISL_139716	Africa	Kenya
A/Maevatanana/4189/2015	EPI_ISL_208484	Africa	Madagascar
A/Maevatanana/4191/2015	EPI_ISL_208485	Africa	Madagascar
A/Maevatanana/4192/2015	EPI_ISL_206504	Africa	Madagascar
A/Maevatanana/4197/2015	EPI_ISL_207929	Africa	Madagascar
A/Mali/025/2016	EPI_ISL_232664	Africa	Mali
A/Mali/030/2017	EPI_ISL_281622	Africa	Mali
A/Mali/033/2016	EPI_ISL_230536	Africa	Mali
A/Mali/047/2016	EPI_ISL_232676	Africa	Mali
A/Mali/075/2017	EPI_ISL_281618	Africa	Mali
A/Mali/082/2017	EPI_ISL_281621	Africa	Mali
A/Mali/084/2016	EPI_ISL_232669	Africa	Mali
A/Mali/085/2016	EPI_ISL_230532	Africa	Mali
A/Mali/085/2017	EPI_ISL_281625	Africa	Mali
A/Mali/087/2017	EPI_ISL_282771	Africa	Mali
A/Mali/088/2017	EPI_ISL_281615	Africa	Mali
A/Mali/090/2017	EPI_ISL_281629	Africa	Mali
A/Mali/091/2017	EPI_ISL_281631	Africa	Mali
A/Mali/095/2016	EPI_ISL_232668	Africa	Mali
A/Mali/096/2016	EPI_ISL_230534	Africa	Mali

A/Mali/098/2016	EPI_ISL_230535	Africa	Mali
A/Mali/100/2016	EPI_ISL_233489	Africa	Mali
A/Mali/101/2017	EPI_ISL_281585	Africa	Mali
A/Mali/110/2016	EPI_ISL_232673	Africa	Mali
A/Mali/115/2016	EPI_ISL_232674	Africa	Mali
A/Mali/199/2017	EPI_ISL_281589	Africa	Mali
A/Mali/252-CI/2015	EPI_ISL_207931	Africa	Mali
A/Mali/6019/2016	EPI_ISL_235014	Africa	Mali
A/Mali/6020/2016	EPI_ISL_232682	Africa	Mali
A/Mali/6063/2016	EPI_ISL_232680	Africa	Mali
A/Mali/6071/2016	EPI_ISL_232683	Africa	Mali
A/Mali/7032/2017	EPI_ISL_282772	Africa	Mali
A/Mombasa/27/2009	EPI_ISL_140395	Africa	Kenya
A/Moramanga/1351/2016	EPI_ISL_230473	Africa	Madagascar
A/Mozambique/333/2017	EPI_ISL_287707	Africa	Mozambique
A/Mozambique/376/2016	EPI_ISL_236217	Africa	Mozambique
A/Nairobi/11/2010	EPI_ISL_140405	Africa	Kenya
A/Nairobi/16/2009	EPI_ISL_140404	Africa	Kenya
A/Nairobi/20/2010	EPI_ISL_140407	Africa	Kenya
A/Nairobi/21/2010	EPI_ISL_140408	Africa	Kenya
A/Nairobi/24/2010	EPI_ISL_140409	Africa	Kenya
A/Nairobi/25/2010	EPI_ISL_140410	Africa	Kenya
A/Nairobi/37/2009	EPI_ISL_140396	Africa	Kenya
A/Nairobi/58/2009	EPI_ISL_139708	Africa	Kenya
A/Nairobi/72/2010	EPI_ISL_140411	Africa	Kenya
A/Nairobi/80/2010	EPI_ISL_140412	Africa	Kenya
A/Nairobi/97/2010	EPI_ISL_140413	Africa	Kenya
A/Nakuru/192/2009	EPI_ISL_139719	Africa	Kenya
A/Niger/5366/2017	EPI_ISL_299845	Africa	Niger
A/Niger/5422/2017	EPI_ISL_299846	Africa	Niger
A/Rwanda/395/2016	EPI_ISL_237822	Africa	Rwanda
A/Rwanda/446/2016	EPI_ISL_232589	Africa	Rwanda
A/Rwanda/483/2016	EPI_ISL_232592	Africa	Rwanda
A/Rwanda/581/2016	EPI_ISL_232134	Africa	Rwanda
A/Rwanda/603/2016	EPI_ISL_232590	Africa	Rwanda
A/Seychelles/106/2009	EPI_ISL_35021	Africa	Seychelles
A/South Africa/2517/2016	EPI_ISL_230453	Africa	South Africa
A/South Africa/3599/2014	EPI_ISL_171814	Africa	South Africa
A/South Africa/3626/2013	EPI_ISL_175880	Africa	South Africa

A/South Africa/4002/2016	EPI_ISL_230465	Africa	South Africa
A/South Africa/4028/2015	EPI_ISL_205287	Africa	South Africa
A/South Africa/4030/2015	EPI_ISL_205294	Africa	South Africa
A/South Africa/4291/2015	EPI_ISL_205295	Africa	South Africa
A/South Africa/4377/2016	EPI_ISL_233066	Africa	South Africa
A/South Africa/5142/2016	EPI_ISL_233064	Africa	South Africa
A/South Africa/5148/2016	EPI_ISL_233065	Africa	South Africa
A/South Africa/5325/2015	EPI_ISL_207384	Africa	South Africa
A/South Africa/R07198/2017	EPI_ISL_283371	Africa	South Africa
A/Tanzania/2082/2015	EPI_ISL_214908	Africa	Tanzania
A/Tanzania/2085/2015	EPI_ISL_214909	Africa	Tanzania
A/Tanzania/2104/2015	EPI_ISL_214171	Africa	Tanzania
A/Tanzania/2109/2015	EPI_ISL_213146	Africa	Tanzania
A/Tanzania/2119/2015	EPI_ISL_216261	Africa	Tanzania
A/Tanzania/2192/2016	EPI_ISL_232603	Africa	Tanzania
A/Tanzania/2226/2016	EPI_ISL_232605	Africa	Tanzania
A/Tanzania/2426/2017	EPI_ISL_298528	Africa	Tanzania
A/Tanzania/2730/2017	EPI_ISL_298522	Africa	Tanzania
A/Tanzania/2767/2015	EPI_ISL_211950	Africa	Tanzania
A/Tanzania/2899/2016	EPI_ISL_232606	Africa	Tanzania
A/Tanzania/2927/2016	EPI_ISL_235339	Africa	Tanzania
A/Tanzania/3866/2015	EPI_ISL_218136	Africa	Tanzania
A/Tanzania/3903/2015	EPI_ISL_214911	Africa	Tanzania
A/Tanzania/4777/2017	EPI_ISL_298526	Africa	Tanzania
A/Tanzania/4778/2017	EPI_ISL_298513	Africa	Tanzania
A/Tanzania/669/2015	EPI_ISL_216262	Africa	Tanzania
A/Tanzania/671/2015	EPI_ISL_207950	Africa	Tanzania
A/Tanzania/689/2016	EPI_ISL_232607	Africa	Tanzania
A/Tanzania/690/2015	EPI_ISL_218137	Africa	Tanzania
A/Toamasina/4159/2015	EPI_ISL_210340	Africa	Madagascar
A/Togo/1023/2017	EPI_ISL_292630	Africa	Togo
A/Togo/1081/2017	EPI_ISL_292623	Africa	Togo
A/Togo/1101/2017	EPI_ISL_292626	Africa	Togo
A/Trans-Nzoia/168/2009	EPI_ISL_139720	Africa	Kenya
A/Tsiroanomandidy/3864/2015	EPI_ISL_218135	Africa	Madagascar
A/Uganda/1625/2014	EPI_ISL_176803	Africa	Uganda
A/Uganda/430/2009	EPI_ISL_62338	Africa	Uganda
A/Uganda/856/2014	EPI_ISL_176806	Africa	Uganda
A/Zambia/0003/2015	EPI_ISL_220967	Africa	Zambia

A/Zambia/0420/2015	EPI_ISL_220966	Africa	Zambia
A/Zambia/302/2015	EPI_ISL_220959	Africa	Zambia
A/Zambia/308/2015	EPI_ISL_220958	Africa	Zambia
A/Zambia/38/2015	EPI_ISL_220969	Africa	Zambia
A/Abu Dhabi/039/2017	EPI_ISL_299801	Asia	United Arab Emirates
A/Abu Dhabi/092/2017	EPI_ISL_307735	Asia	United Arab Emirates
A/Afghanistan/087/2016	EPI_ISL_233088	Asia	Afghanistan
A/Akita/1/2009	EPI_ISL_31855	Asia	Japan
A/Bahrain/1006/2015	EPI_ISL_216234	Asia	Bahrain
A/Bahrain/1420/2015	EPI_ISL_218192	Asia	Bahrain
A/Bahrain/256/2018	EPI_ISL_315809	Asia	Bahrain
A/Bahrain/575/2014	EPI_ISL_173265	Asia	Bahrain
A/Bahrain/602/2014	EPI_ISL_173266	Asia	Bahrain
A/Bangkok/INS424/2010	EPI_ISL_78748	Asia	Thailand
A/Bangkok/INS426/2010	EPI_ISL_78750	Asia	Thailand
A/Bangkok/INS428/2010	EPI_ISL_78752	Asia	Thailand
A/Bangkok/SIMI501/2009	EPI_ISL_181401	Asia	Thailand
A/Bangkok/SIMI502/2010	EPI_ISL_181402	Asia	Thailand
A/Bangkok/SIMI503/2010	EPI_ISL_181403	Asia	Thailand
A/Bangkok/SIMI504/2010	EPI_ISL_181404	Asia	Thailand
A/Bangkok/SIMI505/2010	EPI_ISL_181405	Asia	Thailand
A/Bangkok/SIMI506/2010	EPI_ISL_181406	Asia	Thailand
A/Bangkok/SIMI508/2010	EPI_ISL_181408	Asia	Thailand
A/Bangkok/SIMI511/2010	EPI_ISL_181411	Asia	Thailand
A/Bangladesh/03249/2018	EPI_ISL_333536	Asia	Bangladesh
A/Bangladesh/1097/2015	EPI_ISL_178494	Asia	Bangladesh
A/Bangladesh/11003/2015	EPI_ISL_192153	Asia	Bangladesh
A/Bangladesh/1466/2018	EPI_ISL_330193	Asia	Bangladesh
A/Bangladesh/149/2018	EPI_ISL_330444	Asia	Bangladesh
A/Bangladesh/1496/2018	EPI_ISL_336831	Asia	Bangladesh
A/Bangladesh/1500/2018	EPI_ISL_336809	Asia	Bangladesh
A/Bangladesh/15007/2015	EPI_ISL_201615	Asia	Bangladesh
A/Bangladesh/181/2018	EPI_ISL_330427	Asia	Bangladesh
A/Bangladesh/2002/2015	EPI_ISL_201621	Asia	Bangladesh
A/Bangladesh/2004/2015	EPI_ISL_202374	Asia	Bangladesh
A/Bangladesh/2018/2018	EPI_ISL_346021	Asia	Bangladesh
A/Bangladesh/236/2018	EPI_ISL_333525	Asia	Bangladesh
A/Bangladesh/3006/2015	EPI_ISL_206509	Asia	Bangladesh
A/Bangladesh/3008/2015	EPI_ISL_193002	Asia	Bangladesh

A/Bangladesh/3094/2015	EPI_ISL_194940	Asia	Bangladesh
A/Bangladesh/4004/2015	EPI_ISL_201616	Asia	Bangladesh
A/Bangladesh/5256/2015	EPI_ISL_193606	Asia	Bangladesh
A/Bangladesh/6891/2015	EPI_ISL_192622	Asia	Bangladesh
A/Bangladesh/85006/2015	EPI_ISL_202366	Asia	Bangladesh
A/Bangladesh/9511/2015	EPI_ISL_192624	Asia	Bangladesh
A/Bangladesh/9584/2015	EPI_ISL_192635	Asia	Bangladesh
A/Beijing-Dongcheng/SWL51/2011	EPI_ISL_94552	Asia	China
A/Beijing-Xicheng/SWL1261/2011	EPI_ISL_94564	Asia	China
A/Beijing/01/2009	EPI_ISL_30518	Asia	China
A/CAMBODIA/11/2011	EPI_ISL_101543	Asia	Cambodia
A/Cambodia/1326/2015	EPI_ISL_221606	Asia	Cambodia
A/Cambodia/A0330504/2016	EPI_ISL_239909	Asia	Cambodia
A/Cambodia/A0614502/2016	EPI_ISL_239910	Asia	Cambodia
A/Cambodia/A0621587/2016	EPI_ISL_237864	Asia	Cambodia
A/Cambodia/FSS31314/2016	EPI_ISL_239915	Asia	Cambodia
A/CAMBODIA/Y0630302/2014	EPI_ISL_168842	Asia	Cambodia
A/Chiang Rai/312/2012	EPI_ISL_134826	Asia	Thailand
A/Chongqing/SWL throat swab1/2011	EPI_ISL_94566	Asia	China
A/Daegu/2001/2014	EPI_ISL_172642	Asia	Korea
A/Dundgobi/9746/2009	EPI_ISL_70294	Asia	Mongolia
A/Fujian-Gulou/SWL1103/2011	EPI_ISL_94586	Asia	China
A/Fujian-Gulou/SWL1338/2010_C2	EPI_ISL_334469	Asia	China
A/Fujian-Xinluo/SWL1141/2011	EPI_ISL_94653	Asia	China
A/Fujian-Yanping/SWL1115/2010	EPI_ISL_75084	Asia	China
A/FUKUOKA-C/42/2016	EPI_ISL_270258	Asia	Japan
A/Gansu-Chengguan/SWL579/2011	EPI_ISL_94582	Asia	China
A/Gansu-Ganzhou/SWL33/2012_C1	EPI_ISL_334471	Asia	China
A/Gansu-Ganzhou/SWL33/2012_E2	EPI_ISL_334472	Asia	China
A/Gansu-Ganzhou/SWL34/2012_C1	EPI_ISL_334473	Asia	China
A/Gansu-Ganzhou/SWL34/2012_E2	EPI_ISL_334474	Asia	China
A/GIFU-C/3/2018	EPI_ISL_331259	Asia	Japan
A/Guangdong-Dongwanbendi/SWL1188/2014_C1+C1	EPI_ISL_334435	Asia	China
A/Guangdong-Dongwanbendi/SWL1188/2014_E2+E1	EPI_ISL_334436	Asia	China
A/Guangdong-Jiangcheng/SWL181/2010	EPI_ISL_75866	Asia	China
A/Guangdong-Liwan/SWL1170/2010	EPI_ISL_75871	Asia	China
A/Guangdong-Liwan/SWL172/2010	EPI_ISL_75873	Asia	China
A/Guangdong-Liwan/SWL176/2010	EPI_ISL_75874	Asia	China

A/Guangdong-Wujiang/SWL51/2010	EPI_ISL_75867	Asia	China
A/Guangdong-Xinxing/SWL198/2011	EPI_ISL_94583	Asia	China
A/Guangdong-Yuexiu/SWL1276/2010	EPI_ISL_75872	Asia	China
A/Guangdong-Zhenjiang/SWL165/2010	EPI_ISL_75865	Asia	China
A/Guangdong-Zhenjiang/SWL176/2010	EPI_ISL_75868	Asia	China
A/Guangdong-Zhongshan/SWL1323/2014_C1+C1	EPI_ISL_334437	Asia	China
A/Guangdong-Zhongshan/SWL1323/2014_E2+E1	EPI_ISL_334438	Asia	China
A/Guangdong/02/2009	EPI_ISL_30631	Asia	China
A/Guangdong/03/2009	EPI_ISL_61145	Asia	China
A/Guangdong/2/2009	EPI_ISL_30734	Asia	China
A/Guangdong/SWL3/2009	EPI_ISL_62196	Asia	China
A/Guangzhou/GIRD74/2010	EPI_ISL_135218	Asia	China
A/GuangzhouSB/01/2009	EPI_ISL_61869	Asia	China
A/Guizhou/SWL1/2009	EPI_ISL_73548	Asia	China
A/GUNMA/52/2009	EPI_ISL_64501	Asia	Japan
A/Gyeongbuk/643/2015	EPI_ISL_192068	Asia	Korea
A/Hebei-Yuhua/SWL1187/2011	EPI_ISL_94629	Asia	China
A/Hebei/SWL1/2009	EPI_ISL_73563	Asia	China
A/Heilongjiang-Longsha/SWL1181/2011	EPI_ISL_94652	Asia	China
A/Heilongjiang-Xiangfang/SWL1528/2011	EPI_ISL_94630	Asia	China
A/Heilongjiang-Xiangyang/SWL196/2011	EPI_ISL_94579	Asia	China
A/HIMEJI/L1/2009	EPI_ISL_64503	Asia	Japan
A/HIROSHIMA/19/2013	EPI_ISL_143715	Asia	Japan
A/Hiroshima/230/2009	EPI_ISL_61156	Asia	Japan
A/HIROSHIMA/316/2009	EPI_ISL_64508	Asia	Japan
A/HIROSHIMA/63/2014	EPI_ISL_174813	Asia	Japan
A/Hong Kong/1104/2018	EPI_ISL_319760	Asia	Hong Kong (SAR)
A/Hong Kong/1124/2018	EPI_ISL_319755	Asia	Hong Kong (SAR)
A/Hong Kong/223/2017	EPI_ISL_256090	Asia	Hong Kong (SAR)
A/Hong Kong/26579/2009	EPI_ISL_68772	Asia	Hong Kong (SAR)
A/Hong Kong/3646/2017	EPI_ISL_275657	Asia	Hong Kong (SAR)
A/Hong Kong/415742Md/2009	EPI_ISL_87431	Asia	Hong Kong (SAR)
A/Hong Kong/4988/2017	EPI_ISL_300843	Asia	Hong Kong (SAR)
A/Hong Kong/5008/2013	EPI_ISL_150295	Asia	Hong Kong (SAR)
A/Hong Kong/7572/2014	EPI_ISL_172651	Asia	Hong Kong (SAR)
A/Hong Kong/7573/2014	EPI_ISL_172653	Asia	Hong Kong (SAR)
A/Hong Kong/95/2016	EPI_ISL_224142	Asia	Hong Kong (SAR)
A/Hubei-Hongshan/SWL143/2010	EPI_ISL_75882	Asia	China

A/Hubei-Songzi/SWL1166/2010	EPI_ISL_75879	Asia	China
A/Hubei-Songzi/SWL160/2010	EPI_ISL_75875	Asia	China
A/Hubei-Wuchang/SWL1141/2014_C1+C1	EPI_ISL_334441	Asia	China
A/Hubei-Wuchang/SWL1141/2014_E3+E1	EPI_ISL_334442	Asia	China
A/Hubei-Wuchang/SWL174/2010	EPI_ISL_75881	Asia	China
A/Hubei/99/2009	EPI_ISL_102373	Asia	China
A/Hunan-Furong/SWL410/2011	EPI_ISL_94551	Asia	China
A/Hunan-Jishou/SWL1116/2011	EPI_ISL_94633	Asia	China
A/Hunan-Jishou/SWL1124/2011	EPI_ISL_94654	Asia	China
A/Hunan-Xiangtan/SWL141/2011	EPI_ISL_94576	Asia	China
A/Hunan-Yueyanglou/SWL143/2011	EPI_ISL_94584	Asia	China
A/Hunan-Yuhua/SWL173/2011	EPI_ISL_94585	Asia	China
A/Hunan/SWL throat swab2/2011	EPI_ISL_94562	Asia	China
A/Hunan/SWL throat swab9/2011	EPI_ISL_94567	Asia	China
A/Hunan/SWL3/2009	EPI_ISL_33880	Asia	China
A/India/0322/2017	EPI_ISL_311856	Asia	India
A/India/2192/2012	EPI_ISL_138692	Asia	India
A/India/6427/2014	EPI_ISL_164784	Asia	India
A/India/8900/2015	EPI_ISL_220977	Asia	India
A/India/9358/2017	EPI_ISL_281604	Asia	India
A/India/GWL_DSC/2010	EPI_ISL_104330	Asia	India
A/India/Nag132467/2013	EPI_ISL_146123	Asia	India
A/India/Nsk12388/2012	EPI_ISL_146137	Asia	India
A/India/P1112874/2011	EPI_ISL_146133	Asia	India
A/India/P1114854/2011	EPI_ISL_146135	Asia	India
A/India/P121716/2012	EPI_ISL_146139	Asia	India
A/India/P121717/2012	EPI_ISL_146141	Asia	India
A/India/P121773/2012	EPI_ISL_146143	Asia	India
A/India/P121778/2012	EPI_ISL_146129	Asia	India
A/India/P12946/2012	EPI_ISL_146119	Asia	India
A/India/P131027/2013	EPI_ISL_153079	Asia	India
A/India/P131845/2013	EPI_ISL_146125	Asia	India
A/India/P132194/2013	EPI_ISL_146127	Asia	India
A/India/Pun151508/2015	EPI_ISL_218438	Asia	India
A/Indonesia/1069_S7_L001/2012	EPI_ISL_269906	Asia	Indonesia
A/Indonesia/1239_S17_L001/2012	EPI_ISL_269973	Asia	Indonesia
A/Indonesia/1247_S41_L001/2012	EPI_ISL_269919	Asia	Indonesia
A/Indonesia/1270_S6_L001/2012	EPI_ISL_269977	Asia	Indonesia
A/Indonesia/1279_S66_L001/2012	EPI_ISL_269975	Asia	Indonesia

A/Indonesia/Nihrd-Jpr 189/2016	EPI_ISL_233495	Asia	Indonesia
A/Iraq/10249/2009	EPI_ISL_35012	Asia	Iraq
A/Jeju/837/2017	EPI_ISL_313066	Asia	Korea
A/Jeonbuk/1997/2014	EPI_ISL_172638	Asia	Korea
A/Jeonbuk/1998/2014	EPI_ISL_172639	Asia	Korea
A/Jeonbuk/2005/2014	EPI_ISL_172644	Asia	Korea
A/Jiangsu-Qinhuai/SWL167/2010	EPI_ISL_75085	Asia	China
A/Jiangsu-Xinpu/SWL187/2011	EPI_ISL_94577	Asia	China
A/Jiangxi/SWL throat swab1/2011	EPI_ISL_94568	Asia	China
A/Jilin-Chuanying/SWL1186/2011	EPI_ISL_94581	Asia	China
A/Jilin-Nanguan/SWL181/2010	EPI_ISL_75089	Asia	China
A/KANAGAWA/146/2013	EPI_ISL_153618	Asia	Japan
A/KANAGAWA/149/2013	EPI_ISL_153619	Asia	Japan
A/Kanagawa/163/2014	EPI_ISL_172645	Asia	Japan
A/KANAGAWA/165/2014	EPI_ISL_170429	Asia	Japan
A/KANAGAWA/19/2016	EPI_ISL_223611	Asia	Japan
A/KANAGAWA/AC2/2016	EPI_ISL_258122	Asia	Japan
A/KANAGAWA/AC6/2016	EPI_ISL_258124	Asia	Japan
A/Kazakhstan/159/2016	EPI_ISL_223254	Asia	Kazakhstan
A/Kazakhstan/384/2018	EPI_ISL_311539	Asia	Kazakhstan
A/Kazakhstan/390/2016	EPI_ISL_223258	Asia	Kazakhstan
A/Kazakhstan/52/2015	EPI_ISL_206556	Asia	Kazakhstan
A/Kazakhstan/54/2015	EPI_ISL_206557	Asia	Kazakhstan
A/Kazakhstan/683/2016	EPI_ISL_223271	Asia	Kazakhstan
A/Kazakhstan/72/2016	EPI_ISL_223272	Asia	Kazakhstan
A/Kazakhstan/8014/2018	EPI_ISL_349829	Asia	Kazakhstan
A/Kazakhstan/8079/2018	EPI_ISL_351867	Asia	Kazakhstan
A/KUMAMOTO/1/2016	EPI_ISL_218890	Asia	Japan
A/KUMAMOTO/21/2016	EPI_ISL_221793	Asia	Japan
A/Kuwait/3834/2017	EPI_ISL_307754	Asia	Kuwait
A/Kuwait/7669/2017	EPI_ISL_311855	Asia	Kuwait
A/Kyrgyzstan/49/2015	EPI_ISL_216263	Asia	Kyrgyzstan
A/Laos/0053/2017	EPI_ISL_269931	Asia	Lao
A/Laos/0160/2016	EPI_ISL_223275	Asia	Lao
A/Laos/0176/2017	EPI_ISL_269927	Asia	Lao
A/Laos/0213/2017	EPI_ISL_269959	Asia	Lao
A/Laos/1106/2018	EPI_ISL_354315	Asia	Lao
A/Laos/1187/2014	EPI_ISL_188724	Asia	Lao
A/Laos/1335/2017	EPI_ISL_284085	Asia	Lao

A/Laos/1532/2017	EPI_ISL_284088	Asia	Lao
A/Laos/1698/2018	EPI_ISL_363632	Asia	Lao
A/Laos/1933/2018	EPI_ISL_363634	Asia	Lao
A/Laos/1956/2018	EPI_ISL_363636	Asia	Lao
A/Laos/2069/2018	EPI_ISL_354347	Asia	Lao
A/Laos/2246/2018	EPI_ISL_354348	Asia	Lao
A/Laos/225/2015	EPI_ISL_194927	Asia	Lao
A/Laos/226/2015	EPI_ISL_194937	Asia	Lao
A/Laos/2444/2018	EPI_ISL_364138	Asia	Lao
A/Laos/2581/2018	EPI_ISL_364102	Asia	Lao
A/Laos/2669/2018	EPI_ISL_364133	Asia	Lao
A/Laos/3129/2016	EPI_ISL_240257	Asia	Lao
A/Laos/3299/2018	EPI_ISL_368150	Asia	Lao
A/Laos/3311/2018	EPI_ISL_368151	Asia	Lao
A/Laos/3389/2018	EPI_ISL_368155	Asia	Lao
A/Laos/3416/2018	EPI_ISL_368148	Asia	Lao
A/Laos/3618/2018	EPI_ISL_365941	Asia	Lao
A/Laos/3711/2016	EPI_ISL_248199	Asia	Lao
A/Laos/3795/2017	EPI_ISL_296058	Asia	Lao
A/Laos/4277/2016	EPI_ISL_269924	Asia	Lao
A/Laos/4378/2016	EPI_ISL_269939	Asia	Lao
A/Laos/828/2013	EPI_ISL_159354	Asia	Lao
A/Laos/887/2013	EPI_ISL_159533	Asia	Lao
A/Laos/951/2014	EPI_ISL_172649	Asia	Lao
A/Laos/F2126/2016	EPI_ISL_235169	Asia	Lao
A/Laos/F2843/2016	EPI_ISL_239100	Asia	Lao
A/Laos/JP1252/2009	EPI_ISL_64526	Asia	Lao
A/Lebanon/14L61/2014	EPI_ISL_176844	Asia	Lebanon
A/Lebanon/14L62/2014	EPI_ISL_176845	Asia	Lebanon
A/Lebanon/14L66/2014	EPI_ISL_176846	Asia	Lebanon
A/MACAU/610158/2014	EPI_ISL_166170	Asia	Macao
A/Malaysia/09707/2015	EPI_ISL_209060	Asia	Malaysia
A/Maldives/1499/2017	EPI_ISL_298530	Asia	Maldives
A/Maldives/443/2018	EPI_ISL_330841	Asia	Maldives
A/Mongolia/JP5699/2009	EPI_ISL_64539	Asia	Mongolia
A/Myanmar/13M310/2013	EPI_ISL_172193	Asia	Myanmar
A/Myanmar/14M003/2014	EPI_ISL_173309	Asia	Myanmar
A/Myanmar/14M072/2014	EPI_ISL_173310	Asia	Myanmar
A/Myanmar/14M272/2014	EPI_ISL_173349	Asia	Myanmar

A/Myanmar/14M379/2014	EPI_ISL_173350	Asia	Myanmar
A/Myanmar/14M445/2014	EPI_ISL_173351	Asia	Myanmar
A/Myanmar/JP101/2009	EPI_ISL_61236	Asia	Myanmar
A/Myanmer/14M194/2014	EPI_ISL_173347	Asia	Myanmar
A/Nagasaki/13N057/2014	EPI_ISL_173294	Asia	Japan
A/Nakhonratchasima/217/2017	EPI_ISL_303172	Asia	Thailand
A/Nanjing/1/2009	EPI_ISL_61272	Asia	China
A/Nanjing/1/2010	EPI_ISL_76848	Asia	China
A/NARA/39/2017	EPI_ISL_306505	Asia	Japan
A/Neimenggu-Helingeer/SWL1314/2015_E3	EPI_ISL_334444	Asia	China
A/Nepal/2450/2015	EPI_ISL_212528	Asia	Nepal
A/Nepal/3381/2015	EPI_ISL_206995	Asia	Nepal
A/Nepal/3384/2015	EPI_ISL_207937	Asia	Nepal
A/Nepal/3431/2015	EPI_ISL_206996	Asia	Nepal
A/Nepal/426/2009	EPI_ISL_63241	Asia	Nepal
A/Nepal/810/2015	EPI_ISL_236233	Asia	Nepal
A/NIIGATA/805/2009	EPI_ISL_64548	Asia	Japan
A/Nong Khai/288/2018	EPI_ISL_339868	Asia	Thailand
A/Nonthaburi/214/2017	EPI_ISL_303173	Asia	Thailand
A/Nonthaburi/2398/2014	EPI_ISL_172646	Asia	Thailand
A/NONTHABURI/248/2014	EPI_ISL_166017	Asia	Thailand
A/Nonthaburi/375/2014	EPI_ISL_172652	Asia	Thailand
A/Nonthaburi/393/2015	EPI_ISL_213158	Asia	Thailand
A/Nonthaburi/52/2015	EPI_ISL_195802	Asia	Thailand
A/Oman/1968/2018	EPI_ISL_311517	Asia	Oman
A/Oman/959/2018	EPI_ISL_312951	Asia	Oman
A/Osaka/33/2013	EPI_ISL_393948	Asia	Japan
A/Osaka/488/2009	EPI_ISL_393908	Asia	Japan
A/Osaka/83/2011	EPI_ISL_393947	Asia	Japan
A/Osaka/UT-A01/2013	EPI_ISL_393910	Asia	Japan
A/Pakistan/741/2018	EPI_ISL_302842	Asia	Pakistan
A/Philippines/0937/2017	EPI_ISL_291521	Asia	Philippines
A/Philippines/212/2017	EPI_ISL_273800	Asia	Philippines
A/Philippines/27/2017	EPI_ISL_312594	Asia	Philippines
A/PRACHUAP KHIRI KHAN/332/2013	EPI_ISL_161861	Asia	Thailand
A/Prachuapkhirikhan/334/2016	EPI_ISL_248958	Asia	Thailand
A/SAGA/155/2015	EPI_ISL_211976	Asia	Japan
A/SAITAMA-C/29/2009	EPI_ISL_64559	Asia	Japan

A/SAITAMA-C/45/2014	EPI_ISL_174820	Asia	Japan
A/SAITAMA-C/9/2016	EPI_ISL_214347	Asia	Japan
A/SAITAMA/104/2016	EPI_ISL_240024	Asia	Japan
A/SAKAI/25/2018	EPI_ISL_315206	Asia	Japan
A/SAPPORO/114/2013	EPI_ISL_152927	Asia	Japan
A/SAPPORO/TH1/2013	EPI_ISL_152931	Asia	Japan
A/Shaanxi-Beilin/SWL134/2010	EPI_ISL_75086	Asia	China
A/Shandong-Zhifu/SWL1200/2011	EPI_ISL_94632	Asia	China
A/Shanghai-Baoshan/SWL1989/2015_E1	EPI_ISL_334448	Asia	China
A/Shanghai-Huangpu/SWL12017/2015_E2	EPI_ISL_334460	Asia	China
A/Shanghai-Jingan/SWL1230/2011	EPI_ISL_94580	Asia	China
A/Shanghai-Luwan/SWL1354/2010_C2	EPI_ISL_334475	Asia	China
A/Shanghai-Putuo/SWL1860/2015_E3	EPI_ISL_334464	Asia	China
A/SHIZUOKA-C/99/2013	EPI_ISL_145539	Asia	Japan
A/Sichuan-Chuanshan/SWL118/2011	EPI_ISL_94578	Asia	China
A/Sichuan-Jinniu/SWL446/2009	EPI_ISL_74648	Asia	China
A/Sichuan-Wuhou/SWL4391/2009	EPI_ISL_74649	Asia	China
A/SINGAPORE/12/2012	EPI_ISL_128691	Asia	Singapore
A/Singapore/640/2010	EPI_ISL_90587	Asia	Singapore
A/Singapore/EN555/2013	EPI_ISL_166901	Asia	Singapore
A/Singapore/GP0291/2017	EPI_ISL_269638	Asia	Singapore
A/Singapore/GP0597/2018	EPI_ISL_321720	Asia	Singapore
A/Singapore/GP1338/2017	EPI_ISL_281330	Asia	Singapore
A/Singapore/INFEN-16-0085/2016	EPI_ISL_226994	Asia	Singapore
A/Singapore/INFMOH-16-0037/2016	EPI_ISL_227017	Asia	Singapore
A/Singapore/INFMOH-16-0058/2016	EPI_ISL_227041	Asia	Singapore
A/Singapore/INFMOH-16-0063/2016	EPI_ISL_227045	Asia	Singapore
A/Singapore/INFTT-16-0203/2016	EPI_ISL_226991	Asia	Singapore
A/Singapore/INFTT-16-0425/2016	EPI_ISL_227009	Asia	Singapore
A/Singapore/KK0353/2018	EPI_ISL_321746	Asia	Singapore
A/Singapore/KK0385/2018	EPI_ISL_321748	Asia	Singapore
A/Singapore/KK0398/2017	EPI_ISL_269614	Asia	Singapore
A/Singapore/KK0652/2017	EPI_ISL_269624	Asia	Singapore
A/Singapore/KK066/2010	EPI_ISL_75740	Asia	Singapore
A/Singapore/KK0823/2017	EPI_ISL_281329	Asia	Singapore
A/Singapore/KK0834/2017	EPI_ISL_281339	Asia	Singapore
A/Singapore/KK0958/2017	EPI_ISL_281340	Asia	Singapore
A/Singapore/KK1064/2013	EPI_ISL_166896	Asia	Singapore
A/Singapore/KK1067/2013	EPI_ISL_166897	Asia	Singapore

A/Singapore/KK1073/2013	EPI_ISL_166898	Asia	Singapore
A/Singapore/KK1332/2017	EPI_ISL_292425	Asia	Singapore
A/Singapore/MOH0112/2017	EPI_ISL_269648	Asia	Singapore
A/Singapore/MOH0114/2017	EPI_ISL_269650	Asia	Singapore
A/Singapore/SGH0154/2017	EPI_ISL_269611	Asia	Singapore
A/Singapore/SGH0680/2017	EPI_ISL_281328	Asia	Singapore
A/Singapore/SGH0772/2016	EPI_ISL_240824	Asia	Singapore
A/Singapore/TT0093/2018	EPI_ISL_321700	Asia	Singapore
A/Singapore/TT0169/2017	EPI_ISL_254671	Asia	Singapore
A/Singapore/TT0689/2017	EPI_ISL_269659	Asia	Singapore
A/Singapore/TT1061/2013	EPI_ISL_166900	Asia	Singapore
A/Singapore/TT950/2013	EPI_ISL_166899	Asia	Singapore
A/SONG KHLA/40/2012	EPI_ISL_122585	Asia	Thailand
A/SONG KHLA/416/2012	EPI_ISL_141555	Asia	Thailand
A/SRI LANKA/30/2013	EPI_ISL_148748	Asia	Sri Lanka
A/SRI LANKA/31/2014	EPI_ISL_166024	Asia	Sri Lanka
A/SRI LANKA/61/2013	EPI_ISL_161866	Asia	Sri Lanka
A/Taipei/WR0195T/2009	EPI_ISL_78804	Asia	Taiwan
A/Taiwan/1/2016	EPI_ISL_211983	Asia	Taiwan
A/Taiwan/1018/2011	EPI_ISL_101903	Asia	Taiwan
A/Taiwan/1102/2011	EPI_ISL_101908	Asia	Taiwan
A/Taiwan/1164/2010	EPI_ISL_101898	Asia	Taiwan
A/Taiwan/156/2009	EPI_ISL_65720	Asia	Taiwan
A/Taiwan/1749/2011	EPI_ISL_101910	Asia	Taiwan
A/Taiwan/2883/2011	EPI_ISL_101911	Asia	Taiwan
A/Taiwan/3697/2011	EPI_ISL_101912	Asia	Taiwan
A/Taiwan/3994/2010	EPI_ISL_101899	Asia	Taiwan
A/Taiwan/4501/2011	EPI_ISL_101902	Asia	Taiwan
A/Taiwan/4611/2011	EPI_ISL_101913	Asia	Taiwan
A/Taiwan/5270/2010	EPI_ISL_101900	Asia	Taiwan
A/Taiwan/5506/2011	EPI_ISL_101905	Asia	Taiwan
A/Taiwan/552/2011	EPI_ISL_101907	Asia	Taiwan
A/Taiwan/609/2014	EPI_ISL_172625	Asia	Taiwan
A/Taiwan/612/2014	EPI_ISL_172628	Asia	Taiwan
A/Taiwan/67/2011	EPI_ISL_101906	Asia	Taiwan
A/Taiwan/842/2010	EPI_ISL_101901	Asia	Taiwan
A/Taiwan/T1338/2009	EPI_ISL_33942	Asia	Taiwan
A/Thailand/CU-H9/2009	EPI_ISL_61515	Asia	Thailand
A/Tianjin/SWL2/2009	EPI_ISL_73556	Asia	China

A/Tochigi/10/2010	EPI_ISL_123267	Asia	Japan
A/Tochigi/2/2010	EPI_ISL_123266	Asia	Japan
A/Tochigi/350/2009	EPI_ISL_123264	Asia	Japan
A/TOKYO/17259/2017	EPI_ISL_285927	Asia	Japan
A/Ulaanbaatar/1470/2018	EPI_ISL_320184	Asia	Mongolia
A/Ulaanbaatar/3494/2016	EPI_ISL_257711	Asia	Mongolia
A/Ulaanbaatar/5974/2009	EPI_ISL_65035	Asia	Mongolia
A/Ulsan/53/2015	EPI_ISL_192062	Asia	Korea
A/Vietnam/0125/2015	EPI_ISL_210348	Asia	Vietnam
A/Vietnam/13V H1-1/2013	EPI_ISL_173295	Asia	Vietnam
A/Vietnam/13V H1-4/2013	EPI_ISL_173296	Asia	Vietnam
A/Vietnam/13V H1-5/2013	EPI_ISL_173297	Asia	Vietnam
A/Vietnam/13V H1-6/2013	EPI_ISL_173298	Asia	Vietnam
A/Vietnam/3050/2013	EPI_ISL_189818	Asia	Vietnam
A/Vietnam/6040/2016	EPI_ISL_259851	Asia	Vietnam
A/Vietnam/GHS741/2017	EPI_ISL_292682	Asia	Vietnam
A/Xizang/SWL2/2009	EPI_ISL_73587	Asia	China
A/YAMAGATA/158/2013	EPI_ISL_154136	Asia	Japan
A/YAMAGUCHI/12/2017	EPI_ISL_257916	Asia	Japan
A/YAMANASHI/14332/2014	EPI_ISL_191443	Asia	Japan
A/YOKOHAMA/1017/2009	EPI_ISL_64581	Asia	Japan
A/YOKOHAMA/111/2016	EPI_ISL_217930	Asia	Japan
A/YOKOHAMA/62/2016	EPI_ISL_217925	Asia	Japan
A/YOKOHAMA/98/2016	EPI_ISL_215598	Asia	Japan
A/Yokohama/UT-K101/2012	EPI_ISL_393909	Asia	Japan
A/Zhejiang-Haishu/SWL1289/2010	EPI_ISL_75087	Asia	China
A/Zhejiang/SWL throat swab4/2011	EPI_ISL_94631	Asia	China
A/Zhejiang/X2/2009	EPI_ISL_102043	Asia	China
A/Aarhus/INS240/2009	EPI_ISL_76860	Europe	Denmark
A/Albania/6485/2016	EPI_ISL_224273	Europe	Albania
A/Arkhangelsk/11/2018	EPI_ISL_322394	Europe	Russian Federation
A/Astrakhan/12/2018	EPI_ISL_313578	Europe	Russian Federation
A/Astrakhan/CRIE-7/2014	EPI_ISL_166442	Europe	Russian Federation
A/Athens/INS123/2009	EPI_ISL_75093	Europe	Greece
A/Athens/INS124/2009	EPI_ISL_75094	Europe	Greece
A/Athens/INS153/2009	EPI_ISL_75341	Europe	Greece
A/Athens/INS156/2009	EPI_ISL_75098	Europe	Greece
A/Athens/INS162/2009	EPI_ISL_75103	Europe	Greece
A/Athens/INS165/2009	EPI_ISL_75106	Europe	Greece

A/Athens/INS276/2009	EPI_ISL_76880	Europe	Greece
A/Athens/INS389/2010	EPI_ISL_78733	Europe	Greece
A/Athens/INS390/2010	EPI_ISL_78734	Europe	Greece
A/Athens/INS391/2010	EPI_ISL_78735	Europe	Greece
A/Athens/INS394/2010	EPI_ISL_78736	Europe	Greece
A/Athens/INS396/2010	EPI_ISL_78737	Europe	Greece
A/Athens/INS397/2010	EPI_ISL_78738	Europe	Greece
A/Athens/INS398/2010	EPI_ISL_78739	Europe	Greece
A/Athens/INS411/2010	EPI_ISL_78740	Europe	Greece
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A/Athens/INS413/2010	EPI_ISL_78742	Europe	Greece
A/Athens/INS414/2010	EPI_ISL_78743	Europe	Greece
A/Athens/INS417/2010	EPI_ISL_78744	Europe	Greece
A/Athens/INS419/2010	EPI_ISL_78745	Europe	Greece
A/Athens/INS420/2010	EPI_ISL_78746	Europe	Greece
A/Athens/INS421/2010	EPI_ISL_78747	Europe	Greece
A/Bari/77/2016	EPI_ISL_224202	Europe	Italy
A/Belgorod/01/2009	EPI_ISL_70269	Europe	Russian Federation
A/Berlin/INS430/2010	EPI_ISL_78754	Europe	Germany
A/Bonn/INS178/2010	EPI_ISL_75113	Europe	Germany
A/Bonn/INS280/2009	EPI_ISL_76883	Europe	Germany
A/Bourgogne/1774/2017	EPI_ISL_290228	Europe	France
A/Bourgogne/344/2018	EPI_ISL_305387	Europe	France
A/Bretagne/1580/2018	EPI_ISL_311462	Europe	France
A/Bretagne/1593/2017	EPI_ISL_290210	Europe	France
A/Bretagne/1939/2017	EPI_ISL_293037	Europe	France
A/Brussels/INS206/2009	EPI_ISL_76885	Europe	Belgium
A/Bulgaria/010/2016	EPI_ISL_208463	Europe	Bulgaria
A/Cardiff/5622/2018	EPI_ISL_334056	Europe	United Kingdom
A/Centre/1920/2017	EPI_ISL_293035	Europe	France
A/Centre/283/2016	EPI_ISL_216320	Europe	France
A/Champagne_Ardenne/1204/2018	EPI_ISL_306575	Europe	France
A/Champagne_Ardenne/1773/2017	EPI_ISL_290227	Europe	France
A/Champagne_Ardenne/2562/2015	EPI_ISL_216460	Europe	France
A/Champagne_Ardenne/2591/2018	EPI_ISL_335324	Europe	France
A/Champagne_Ardenne/350/2016	EPI_ISL_216323	Europe	France
A/Cheboksary/IIV-92/2011	EPI_ISL_97359	Europe	Russian Federation
A/Cwmbran/4014/2018	EPI_ISL_333638	Europe	United Kingdom
A/Czech Republic/1/2011	EPI_ISL_89373	Europe	Czech Republic

A/Czech Republic/111/2011	EPI_ISL_108485	Europe	Czech Republic
A/Czech Republic/112/2011	EPI_ISL_108500	Europe	Czech Republic
A/Denmark/59/2018	EPI_ISL_302067	Europe	Denmark
A/Dijon/661/2018	EPI_ISL_305474	Europe	France
A/Dnipropetrovsk/437/2015	EPI_ISL_192045	Europe	Ukraine
A/Ekaterinburg/RII12/2016	EPI_ISL_233974	Europe	Russian Federation
A/England/129/2014	EPI_ISL_202968	Europe	United Kingdom
A/England/13/2014	EPI_ISL_202961	Europe	United Kingdom
A/England/130/2018	EPI_ISL_303399	Europe	United Kingdom
A/England/138/2017	EPI_ISL_292258	Europe	United Kingdom
A/England/14/2014	EPI_ISL_202963	Europe	United Kingdom
A/England/150/2015	EPI_ISL_212222	Europe	United Kingdom
A/England/178/2014	EPI_ISL_202970	Europe	United Kingdom
A/England/20/2014	EPI_ISL_202964	Europe	United Kingdom
A/England/20/2017	EPI_ISL_270587	Europe	United Kingdom
A/England/204/2009	EPI_ISL_101312	Europe	United Kingdom
A/England/220/2009	EPI_ISL_32516	Europe	United Kingdom
A/England/233/2016	EPI_ISL_241169	Europe	United Kingdom
A/England/240/2016	EPI_ISL_241174	Europe	United Kingdom
A/England/254/2009	EPI_ISL_101382	Europe	United Kingdom
A/England/256/2009	EPI_ISL_101384	Europe	United Kingdom
A/England/305/2016	EPI_ISL_241192	Europe	United Kingdom
A/England/328/2009	EPI_ISL_93045	Europe	United Kingdom
A/England/334/2016	EPI_ISL_241201	Europe	United Kingdom
A/England/344/2015	EPI_ISL_212224	Europe	United Kingdom
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A/England/34700586/2013	EPI_ISL_202956	Europe	United Kingdom
A/England/353/2015	EPI_ISL_203378	Europe	United Kingdom
A/England/354/2014	EPI_ISL_212270	Europe	United Kingdom
A/England/354/2015	EPI_ISL_212228	Europe	United Kingdom
A/England/357/2015	EPI_ISL_203381	Europe	United Kingdom
A/England/365/2009	EPI_ISL_93060	Europe	United Kingdom
A/England/376/2015	EPI_ISL_212236	Europe	United Kingdom
A/England/394/2014	EPI_ISL_202975	Europe	United Kingdom
A/England/40380620/2014	EPI_ISL_202965	Europe	United Kingdom
A/England/40800135/2014	EPI_ISL_202969	Europe	United Kingdom
A/England/414/2009	EPI_ISL_101473	Europe	United Kingdom
A/England/41420345/2014	EPI_ISL_202977	Europe	United Kingdom
A/England/41420346/2014	EPI_ISL_202978	Europe	United Kingdom

A/England/41420347/2014	EPI_ISL_202979	Europe	United Kingdom
A/England/41420351/2014	EPI_ISL_202982	Europe	United Kingdom
A/England/41420353/2014	EPI_ISL_202983	Europe	United Kingdom
A/England/41420354/2014	EPI_ISL_202984	Europe	United Kingdom
A/England/41420356/2014	EPI_ISL_202986	Europe	United Kingdom
A/England/41420359/2014	EPI_ISL_202988	Europe	United Kingdom
A/England/41420361/2014	EPI_ISL_202989	Europe	United Kingdom
A/England/416/2009	EPI_ISL_93077	Europe	United Kingdom
A/England/417/2015	EPI_ISL_240945	Europe	United Kingdom
A/England/41780007/2014	EPI_ISL_202991	Europe	United Kingdom
A/England/422/2015	EPI_ISL_240950	Europe	United Kingdom
A/England/427/2015	EPI_ISL_240958	Europe	United Kingdom
A/England/439/2014	EPI_ISL_212217	Europe	United Kingdom
A/England/472/2016	EPI_ISL_241152	Europe	United Kingdom
A/England/476/2014	EPI_ISL_202976	Europe	United Kingdom
A/England/527/2009	EPI_ISL_129378	Europe	United Kingdom
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A/England/55120205/2015	EPI_ISL_240936	Europe	United Kingdom
A/England/55240293/2015	EPI_ISL_212245	Europe	United Kingdom
A/England/55240295/2015	EPI_ISL_212246	Europe	United Kingdom
A/England/55340398/2015	EPI_ISL_240946	Europe	United Kingdom
A/England/6/2014	EPI_ISL_202960	Europe	United Kingdom
A/England/60180752/2016	EPI_ISL_212258	Europe	United Kingdom
A/England/60620149/2016	EPI_ISL_241218	Europe	United Kingdom
A/England/60880101/2016	EPI_ISL_241406	Europe	United Kingdom
A/England/61240082/2016	EPI_ISL_241279	Europe	United Kingdom
A/England/621/2013	EPI_ISL_202953	Europe	United Kingdom
A/England/624/2013	EPI_ISL_202955	Europe	United Kingdom
A/England/649/2016	EPI_ISL_241454	Europe	United Kingdom
A/England/660/2013	EPI_ISL_202957	Europe	United Kingdom
A/England/665/2013	EPI_ISL_202958	Europe	United Kingdom
A/England/673/2013	EPI_ISL_202959	Europe	United Kingdom
A/England/68/2014	EPI_ISL_202967	Europe	United Kingdom
A/England/684/2013	EPI_ISL_241200	Europe	United Kingdom
A/England/689/2016	EPI_ISL_241493	Europe	United Kingdom
A/England/69/2017	EPI_ISL_286851	Europe	United Kingdom
A/England/691/2016	EPI_ISL_241250	Europe	United Kingdom
A/England/699/2018	EPI_ISL_338421	Europe	United Kingdom
A/England/706/2018	EPI_ISL_341232	Europe	United Kingdom

A/England/708/2016	EPI_ISL_241269	Europe	United Kingdom
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A/England/718/2018	EPI_ISL_338414	Europe	United Kingdom
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A/England/731/2018	EPI_ISL_351379	Europe	United Kingdom
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A/England/74640396/2017	EPI_ISL_291005	Europe	United Kingdom
A/England/74700487/2017	EPI_ISL_291013	Europe	United Kingdom
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A/England/74860301/2017	EPI_ISL_291030	Europe	United Kingdom
A/England/75/2017	EPI_ISL_291012	Europe	United Kingdom
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A/England/75260793/2017	EPI_ISL_292281	Europe	United Kingdom
A/England/76/2017	EPI_ISL_291014	Europe	United Kingdom
A/England/766/2009	EPI_ISL_93106	Europe	United Kingdom
A/England/80/2017	EPI_ISL_291039	Europe	United Kingdom
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A/England/88/2016	EPI_ISL_241126	Europe	United Kingdom
A/England/902/2009	EPI_ISL_93098	Europe	United Kingdom
A/England/941/2009	EPI_ISL_93109	Europe	United Kingdom
A/England/H093900113/2009	EPI_ISL_93113	Europe	United Kingdom
A/England/H094220579/2009	EPI_ISL_93103	Europe	United Kingdom
A/England/XFL00364/2009	EPI_ISL_129388	Europe	United Kingdom
A/England/XFL00482/2009	EPI_ISL_101403	Europe	United Kingdom
A/Frankfurt/INS402/2010	EPI_ISL_78760	Europe	Germany
A/Frankfurt/INS403/2010	EPI_ISL_78761	Europe	Germany
A/Gavle/2/2014	EPI_ISL_156997	Europe	Sweden
A/Gavle/3/2014	EPI_ISL_156998	Europe	Sweden
A/Germany/40/2014	EPI_ISL_173260	Europe	Germany
A/Germany/51/2014	EPI_ISL_173272	Europe	Germany
A/Halmstad/1/2013	EPI_ISL_150118	Europe	Sweden
A/Halmstad/4/2017	EPI_ISL_291396	Europe	Sweden
A/Haute_Normandie/1859/2017	EPI_ISL_294127	Europe	France
A/Haute_Normandie/1945/2017	EPI_ISL_293038	Europe	France
A/Haute_Normandie/2000/2017	EPI_ISL_297439	Europe	France
A/Haute_Normandie/973/2018	EPI_ISL_305399	Europe	France
A/IIV-Moscow/155/2015	EPI_ISL_207504	Europe	Russian Federation
A/IIV-Moscow/168/2015	EPI_ISL_207513	Europe	Russian Federation
A/IIV-Moscow/178/2015	EPI_ISL_207520	Europe	Russian Federation

A/IIV-Moscow/181/2015	EPI_ISL_207522	Europe	Russian Federation
A/IIV-Moscow/183/2015	EPI_ISL_207524	Europe	Russian Federation
A/IIV-Moscow/185/2015	EPI_ISL_207525	Europe	Russian Federation
A/IIV-Moscow/202/2015	EPI_ISL_207538	Europe	Russian Federation
A/Joshkar-Ola/CRIE-BLP/2011	EPI_ISL_97441	Europe	Russian Federation
A/Karasuk/01/2010	EPI_ISL_68134	Europe	Russian Federation
A/Kazan/CRIE-02/2013	EPI_ISL_156274	Europe	Russian Federation
A/Kazan/CRIE-04/2013	EPI_ISL_156278	Europe	Russian Federation
A/Kemerovo/RII-3915S/2018	EPI_ISL_322346	Europe	Russian Federation
A/Khabarovsk/49/2018	EPI_ISL_337114	Europe	Russian Federation
A/Krasnodar/421/2017	EPI_ISL_331308	Europe	Russian Federation
A/Lisbon/137/2013	EPI_ISL_156806	Europe	Portugal
A/Llanelli/0228/2018	EPI_ISL_331248	Europe	United Kingdom
A/Llanelli/9467/2018	EPI_ISL_331389	Europe	United Kingdom
A/Lund/4/2018	EPI_ISL_302831	Europe	Sweden
A/Macedonia/283/2018	EPI_ISL_309507	Europe	Macedonia
A/Madrid/INS113/2009	EPI_ISL_75138	Europe	Spain
A/Madrid/INS131/2009	EPI_ISL_75140	Europe	Spain
A/Madrid/INS222/2009	EPI_ISL_76897	Europe	Spain
A/Malmoe/1/2014	EPI_ISL_155009	Europe	Sweden
A/Moscow/107/2015	EPI_ISL_193300	Europe	Russian Federation
A/Moscow/238/2015	EPI_ISL_216272	Europe	Russian Federation
A/Moscow/240/2015	EPI_ISL_216274	Europe	Russian Federation
A/Moscow/243/2015	EPI_ISL_216277	Europe	Russian Federation
A/Moscow/IIV-33/2010	EPI_ISL_86197	Europe	Russian Federation
A/Moscow/IIV-45/2012	EPI_ISL_127690	Europe	Russian Federation
A/Moscow/IIV-83/2011	EPI_ISL_93345	Europe	Russian Federation
A/Moscow/IIV03/2009	EPI_ISL_31497	Europe	Russian Federation
A/Moscow/RII-779S/2018	EPI_ISL_297764	Europe	Russian Federation
A/Moscow/WR1866N/2009	EPI_ISL_78851	Europe	Russian Federation
A/Mykop/2353/2018	EPI_ISL_330782	Europe	Russian Federation
A/Netherlands/2243/2009	EPI_ISL_76464	Europe	Netherlands
A/Netherlands/2442b/2009	EPI_ISL_76466	Europe	Netherlands
A/Netherlands/3523/2017	EPI_ISL_291992	Europe	Netherlands
A/Netherlands/3792/2016	EPI_ISL_241361	Europe	Netherlands
A/Nizhnii Novgorod/CRIE-BLM/2011	EPI_ISL_97440	Europe	Russian Federation
A/Nizhnii Novgorod/CRIE-NGV/2010	EPI_ISL_97439	Europe	Russian Federation
A/Nord_Pas_de_Calais/1473/2018	EPI_ISL_306578	Europe	France
A/Nord_Pas_de_Calais/250/2016	EPI_ISL_216319	Europe	France

A/Nord_Pas_de_Calais/526/2018	EPI_ISL_302312	Europe	France
A/Novosibirsk/02/2009	EPI_ISL_66840	Europe	Russian Federation
A/Novosibirsk/KSH/2011	EPI_ISL_102003	Europe	Russian Federation
A/Odessa/166/2017	EPI_ISL_268428	Europe	Ukraine
A/Odessa/65/2016	EPI_ISL_216205	Europe	Ukraine
A/Odessa/692/2016	EPI_ISL_230458	Europe	Ukraine
A/Orenburg/IIV-13/2010	EPI_ISL_73804	Europe	Russian Federation
A/Paris/1229/2017	EPI_ISL_266852	Europe	France
A/Paris/1284/2016	EPI_ISL_218989	Europe	France
A/Paris/1529/2017	EPI_ISL_291153	Europe	France
A/Paris/1576/2016	EPI_ISL_218974	Europe	France
A/Paris/1578/2017	EPI_ISL_290208	Europe	France
A/Paris/1585/2017	EPI_ISL_290209	Europe	France
A/Paris/1700/2017	EPI_ISL_290219	Europe	France
A/Paris/1725/2017	EPI_ISL_294126	Europe	France
A/Paris/181/2016	EPI_ISL_216316	Europe	France
A/Paris/2057/2016	EPI_ISL_221806	Europe	France
A/Paris/234/2016	EPI_ISL_216318	Europe	France
A/Paris/2584/2016	EPI_ISL_233385	Europe	France
A/Paris/2588/2016	EPI_ISL_233388	Europe	France
A/Paris/2591/2009	EPI_ISL_30754	Europe	France
A/Paris/388/2016	EPI_ISL_216324	Europe	France
A/Pays_de_Loire/1184/2018	EPI_ISL_305483	Europe	France
A/Pays_de_Loire/1614/2018	EPI_ISL_311463	Europe	France
A/Pays_de_Loire/482/2018	EPI_ISL_302309	Europe	France
A/Pays_de_Loire/490/2018	EPI_ISL_297458	Europe	France
A/Penarth/6242/2018	EPI_ISL_331351	Europe	United Kingdom
A/Picardie/1225/2018	EPI_ISL_305485	Europe	France
A/Picardie/796/2016	EPI_ISL_218733	Europe	France
A/Pontyclun/1660/2018	EPI_ISL_333208	Europe	United Kingdom
A/Rostov-on-Don/3171/2017	EPI_ISL_290990	Europe	Russian Federation
A/Rostov-On-Don/3171/2017	EPI_ISL_314522	Europe	Russian Federation
A/Rostov-on-Don/3196/2017	EPI_ISL_282528	Europe	Russian Federation
A/Russia/4/2009	EPI_ISL_67085	Europe	Russian Federation
A/Saint-Petersburg/RII-334S/2018	EPI_ISL_337128	Europe	Russian Federation
A/Saint-Petersburg/RII1530M/2016	EPI_ISL_234005	Europe	Russian Federation
A/Saint-Petersburg/RII48/2016	EPI_ISL_234023	Europe	Russian Federation
A/Saint-Petersburg/RII579S/2015	EPI_ISL_207557	Europe	Russian Federation
A/Scotland/10/2009	EPI_ISL_101649	Europe	United Kingdom

A/Skovde/4/2017	EPI_ISL_285987	Europe	Sweden
A/St Petersburg/1/2015	EPI_ISL_218153	Europe	Russian Federation
A/St Petersburg/350/2015	EPI_ISL_218152	Europe	Russian Federation
A/St Petersburg/46/2015	EPI_ISL_192117	Europe	Russian Federation
A/St Petersburg/61/2015	EPI_ISL_192115	Europe	Russian Federation
A/St Petersburg/RII-477/2018	EPI_ISL_330040	Europe	Russian Federation
A/St Petersburg/RII-563/2018	EPI_ISL_346015	Europe	Russian Federation
A/St. Petersburg/100/2011	EPI_ISL_89916	Europe	Russian Federation
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A/St. Petersburg/204/2010	EPI_ISL_79365	Europe	Russian Federation
A/Stockholm/1/2012	EPI_ISL_149711	Europe	Sweden
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A/Sweden/82/2017	EPI_ISL_292041	Europe	Sweden
A/Sweden/96/2018	EPI_ISL_335548	Europe	Sweden
A/Switzerland/2656/2017	EPI_ISL_315812	Europe	Switzerland
A/Tallinn/INS182/2010	EPI_ISL_75152	Europe	Estonia
A/Tallinn/INS183/2010	EPI_ISL_75153	Europe	Estonia
A/Tallinn/INS372/2009	EPI_ISL_78781	Europe	Estonia
A/Tallinn/INS373/2010	EPI_ISL_78782	Europe	Estonia
A/Tessenderlo/INS192/2009	EPI_ISL_75160	Europe	Belgium
A/Tomsk/IIV-19/2012	EPI_ISL_116258	Europe	Russian Federation
A/Tula/11/2018	EPI_ISL_322410	Europe	Russian Federation
A/Tula/CRIE-SIA/2011	EPI_ISL_95840	Europe	Russian Federation
A/Tula/RII04/2016	EPI_ISL_233973	Europe	Russian Federation
A/Ukraine/6/2016	EPI_ISL_216200	Europe	Ukraine
A/Uppsala/1/2014	EPI_ISL_154974	Europe	Sweden
A/Uppsala/3/2014	EPI_ISL_156916	Europe	Sweden
A/Uppsala/4/2016	EPI_ISL_220463	Europe	Sweden
A/Uppsala/5/2014	EPI_ISL_157114	Europe	Sweden
A/Vienna/INS179/2010	EPI_ISL_75162	Europe	Austria
A/Vienna/INS368/2010	EPI_ISL_78784	Europe	Austria
A/Vladimir/IIV-35/2011	EPI_ISL_93346	Europe	Russian Federation
A/Vladivistok/7/2010	EPI_ISL_87285	Europe	Russian Federation
A/Vladivostok/28/2012	EPI_ISL_128296	Europe	Russian Federation
A/Volgograd/CRIE-4/2014	EPI_ISL_166412	Europe	Russian Federation

A/Volgograd/CRIE-DMV/2011	EPI_ISL_97442	Europe	Russian Federation
A/Voronezh/01/2011	EPI_ISL_89925	Europe	Russian Federation
A/Zaporizza/417/2013	EPI_ISL_145501	Europe	Ukraine
A/Alabama/03/2010	EPI_ISL_73400	North America	United States
A/Alabama/10/2018	EPI_ISL_300041	North America	United States
A/Alaska/01/2010	EPI_ISL_71344	North America	United States
A/Alaska/07/2018	EPI_ISL_302952	North America	United States
A/Alaska/263/2015	EPI_ISL_203590	North America	United States
A/Alaska/37/2014	EPI_ISL_171853	North America	United States
A/Alaska/38/2014	EPI_ISL_171851	North America	United States
A/Alaska/45/2018	EPI_ISL_315078	North America	United States
A/Arizona/01/2011	EPI_ISL_88059	North America	United States
A/Arizona/15/2017	EPI_ISL_259820	North America	United States
A/Arizona/42/2016	EPI_ISL_221069	North America	United States
A/Arkansas/03/2018	EPI_ISL_300035	North America	United States
A/Boston/146/2009	EPI_ISL_75348	North America	United States
A/Brownsville/31OS/2009	EPI_ISL_63967	North America	United States
A/Brownsville/37OS/2009	EPI_ISL_63979	North America	United States
A/Brownsville/43H/2009	EPI_ISL_63978	North America	United States
A/California/01/2014	EPI_ISL_157476	North America	United States
A/California/05/2010	EPI_ISL_73401	North America	United States
A/California/06/2014	EPI_ISL_158707	North America	United States
A/California/07/2009	EPI_ISL_203615	North America	United States
A/California/115/2015	EPI_ISL_205482	North America	United States
A/California/121/2017	EPI_ISL_287697	North America	United States
A/California/123/2017	EPI_ISL_287696	North America	United States
A/California/128/2015	EPI_ISL_208469	North America	United States
A/California/134/2017	EPI_ISL_288563	North America	United States
A/California/14/2011	EPI_ISL_88065	North America	United States
A/California/142/2017	EPI_ISL_290757	North America	United States
A/California/17/2011	EPI_ISL_89892	North America	United States
A/California/171/2016	EPI_ISL_264360	North America	United States
A/California/20/2011	EPI_ISL_94669	North America	United States
A/California/21/2011	EPI_ISL_94670	North America	United States
A/California/26/2016	EPI_ISL_213269	North America	United States
A/California/31/2017	EPI_ISL_255940	North America	United States
A/California/33/2017	EPI_ISL_256089	North America	United States
A/California/46/2017	EPI_ISL_257790	North America	United States
A/California/55/2014	EPI_ISL_192124	North America	United States

A/California/56/2014	EPI_ISL_188708	North America	United States
A/California/56/2016	EPI_ISL_216192	North America	United States
A/California/59/2013	EPI_ISL_157072	North America	United States
A/California/81/2018	EPI_ISL_332629	North America	United States
A/California/92/2014	EPI_ISL_188709	North America	United States
A/California/VRDL1/2010	EPI_ISL_76739	North America	United States
A/California/VRDL10/2010	EPI_ISL_75114	North America	United States
A/California/VRDL11/2010	EPI_ISL_75118	North America	United States
A/California/VRDL13/2010	EPI_ISL_75120	North America	United States
A/California/VRDL14/2010	EPI_ISL_75121	North America	United States
A/California/VRDL2/2010	EPI_ISL_76740	North America	United States
A/California/VRDL9/2009	EPI_ISL_68133	North America	United States
A/Canada MB/RV1975/2009	EPI_ISL_32649	North America	United States
A/Canada MB/RV2004/2009	EPI_ISL_86289	North America	United States
A/Canada MB/RV2018/2010	EPI_ISL_86300	North America	United States
A/Canada NB/RV2478/2009	EPI_ISL_86367	North America	United States
A/Canada ON/RV2015/2010	EPI_ISL_86396	North America	United States
A/Colorado/02/2010	EPI_ISL_71360	North America	United States
A/Colorado/07/2014	EPI_ISL_163674	North America	United States
A/Colorado/11/2010	EPI_ISL_88067	North America	United States
A/Colorado/26/2017	EPI_ISL_290733	North America	United States
A/Colorado/35/2015	EPI_ISL_210282	North America	United States
A/Connecticut/07/2017	EPI_ISL_256905	North America	United States
A/Costa Rica/5802/2013	EPI_ISL_150617	North America	Costa Rica
A/Costa Rica/7688/2015	EPI_ISL_215030	North America	Costa Rica
A/Costa Rica/7890/2015	EPI_ISL_218181	North America	Costa Rica
A/Craven/WR0019/2009	EPI_ISL_61793	North America	United States
A/Delaware/04/2011	EPI_ISL_88072	North America	United States
A/Delaware/06/2011	EPI_ISL_88073	North America	United States
A/Delaware/08/2011	EPI_ISL_88075	North America	United States
A/District Of Columbia/02/2014	EPI_ISL_233734	North America	United States
A/District Of Columbia/10/2018	EPI_ISL_309036	North America	United States
A/Dominica/432/2015	EPI_ISL_193592	North America	Dominica
A/Dominican Republic/7293/2013	EPI_ISL_145504	North America	Dominican Republic
A/Dominican Republic/9270/2015	EPI_ISL_194833	North America	Dominican Republic
A/El Salvador/1077/2016	EPI_ISL_240243	North America	El Salvador
A/El Salvador/442/2016	EPI_ISL_232711	North America	El Salvador
A/El Salvador/713/2018	EPI_ISL_331146	North America	El Salvador
A/Florida/01/2014	EPI_ISL_154792	North America	United States

A/Florida/02/2010	EPI_ISL_71369	North America	United States
A/Florida/06/2012	EPI_ISL_117054	North America	United States
A/Florida/47/2015	EPI_ISL_188712	North America	United States
A/Florida/56/2015	EPI_ISL_193301	North America	United States
A/Florida/62/2014	EPI_ISL_171852	North America	United States
A/Florida/66/2015	EPI_ISL_197569	North America	United States
A/Georgia/04/2010	EPI_ISL_73417	North America	United States
A/Georgia/15/2015	EPI_ISL_210289	North America	United States
A/Guatemala/122/2016	EPI_ISL_233080	North America	Guatemala
A/Guatemala/209/2018	EPI_ISL_330196	North America	Guatemala
A/Guatemala/24/2016	EPI_ISL_233538	North America	Guatemala
A/Guatemala/616/2018	EPI_ISL_330174	North America	Guatemala
A/Guatemala/86/2016	EPI_ISL_233539	North America	Guatemala
A/Haiti/1790/2013	EPI_ISL_145496	North America	Haiti
A/Hawaii/03/2013	EPI_ISL_156762	North America	United States
A/Hawaii/19/2018	EPI_ISL_305225	North America	United States
A/Hawaii/20/2017	EPI_ISL_268496	North America	United States
A/Hawaii/24/2018	EPI_ISL_305226	North America	United States
A/Hawaii/30/2015	EPI_ISL_189822	North America	United States
A/Hawaii/41/2015	EPI_ISL_192147	North America	United States
A/Hawaii/43/2017	EPI_ISL_282768	North America	United States
A/Hawaii/64/2014	EPI_ISL_171846	North America	United States
A/Hawaii/82/2015	EPI_ISL_210292	North America	United States
A/Honduras/0198/2017	EPI_ISL_269923	North America	Honduras
A/Honduras/1875/2018	EPI_ISL_314529	North America	Honduras
A/Honduras/2586/2018	EPI_ISL_335907	North America	Honduras
A/Houston/10H/2009	EPI_ISL_63950	North America	United States
A/Houston/5H/2009	EPI_ISL_63943	North America	United States
A/Idaho/06/2016	EPI_ISL_214986	North America	United States
A/Idaho/39/2015	EPI_ISL_208479	North America	United States
A/Illinois/13/2016	EPI_ISL_221233	North America	United States
A/Illinois/21/2015	EPI_ISL_203290	North America	United States
A/Illinois/26/2017	EPI_ISL_259823	North America	United States
A/Illinois/28/2015	EPI_ISL_211718	North America	United States
A/Indiana/04/2011	EPI_ISL_88085	North America	United States
A/Indiana/10/2017	EPI_ISL_249931	North America	United States
A/Indiana/33/2015	EPI_ISL_207928	North America	United States
A/Indiana/38/2016	EPI_ISL_221277	North America	United States
A/Iowa/01/2010	EPI_ISL_70323	North America	United States

A/Iowa/08/2018	EPI_ISL_302873	North America	United States
A/Iowa/09/2017	EPI_ISL_256355	North America	United States
A/Iowa/10/2017	EPI_ISL_256356	North America	United States
A/Iowa/19/2014	EPI_ISL_170147	North America	United States
A/Iowa/24/2014	EPI_ISL_173273	North America	United States
A/Iowa/25/2014	EPI_ISL_173268	North America	United States
A/Iowa/25/2018	EPI_ISL_307729	North America	United States
A/Iowa/26/2014	EPI_ISL_173274	North America	United States
A/Iowa/27/2014	EPI_ISL_173264	North America	United States
A/Jamaica/5010/2018	EPI_ISL_345994	North America	Jamaica
A/Jamaica/613/2016	EPI_ISL_233522	North America	Jamaica
A/Jamaica/7765/2018	EPI_ISL_342319	North America	Jamaica
A/Kentucky/28/2018	EPI_ISL_331417	North America	United States
A/Louisiana/03/2015	EPI_ISL_192125	North America	United States
A/Louisiana/07/2013	EPI_ISL_150042	North America	United States
A/Louisiana/08/2013	EPI_ISL_150043	North America	United States
A/Louisiana/10/2013	EPI_ISL_150298	North America	United States
A/Louisiana/11/2013	EPI_ISL_150297	North America	United States
A/Louisiana/12/2013	EPI_ISL_150296	North America	United States
A/Louisiana/13/2013	EPI_ISL_151838	North America	United States
A/Louisiana/34/2013	EPI_ISL_155018	North America	United States
A/Louisiana/41/2013	EPI_ISL_159528	North America	United States
A/Maine/01/2016	EPI_ISL_215054	North America	United States
A/Maine/04/2011	EPI_ISL_88099	North America	United States
A/Martinique/2084/2015	EPI_ISL_195810	North America	Martinique
A/Maryland/03/2011	EPI_ISL_88100	North America	United States
A/Maryland/04/2011	EPI_ISL_88101	North America	United States
A/Maryland/04/2014	EPI_ISL_157859	North America	United States
A/Maryland/05/2011	EPI_ISL_88102	North America	United States
A/Maryland/06/2011	EPI_ISL_88103	North America	United States
A/Maryland/07/2011	EPI_ISL_88104	North America	United States
A/Maryland/08/2011	EPI_ISL_88105	North America	United States
A/Maryland/13/2012	EPI_ISL_128402	North America	United States
A/Maryland/20/2013	EPI_ISL_154243	North America	United States
A/Maryland/28/2016	EPI_ISL_273767	North America	United States
A/Maryland/57/2018	EPI_ISL_333824	North America	United States
A/Maryland/95/2017	EPI_ISL_296219	North America	United States
A/Massachusetts/06/2017	EPI_ISL_268433	North America	United States
A/Massachusetts/15/2013	EPI_ISL_153134	North America	United States

A/Massachusetts/30/2015	EPI_ISL_203611	North America	United States
A/Massachusetts/31/2015	EPI_ISL_208487	North America	United States
A/Mexico City/019/2009	EPI_ISL_76071	North America	Mexico
A/Mexico City/WR1704T/2009	EPI_ISL_78845	North America	Mexico
A/Mexico/1244/2018	EPI_ISL_313564	North America	Mexico
A/Mexico/1247/2018	EPI_ISL_313565	North America	Mexico
A/Mexico/1374/2015	EPI_ISL_200996	North America	Mexico
A/Mexico/1985/2018	EPI_ISL_332988	North America	Mexico
A/Mexico/1986/2017	EPI_ISL_275669	North America	Mexico
A/Mexico/1991/2018	EPI_ISL_332989	North America	Mexico
A/Mexico/2188/2018	EPI_ISL_332221	North America	Mexico
A/Mexico/254/2012	EPI_ISL_103741	North America	Mexico
A/Mexico/27/2016	EPI_ISL_259866	North America	Mexico
A/Mexico/2964/2009	EPI_ISL_66702	North America	Mexico
A/Mexico/3723/2011	EPI_ISL_103740	North America	Mexico
A/Mexico/3752/2011	EPI_ISL_105062	North America	Mexico
A/Mexico/4281/2016	EPI_ISL_238775	North America	Mexico
A/Michigan/03/2011	EPI_ISL_94671	North America	United States
A/Michigan/03/2016	EPI_ISL_210296	North America	United States
A/Michigan/15/2016	EPI_ISL_224148	North America	United States
A/Michigan/277/2017	EPI_ISL_277882	North America	United States
A/Michigan/280/2017	EPI_ISL_281591	North America	United States
A/Michigan/45/2015	EPI_ISL_200780	North America	United States
A/Michigan/57/2015	EPI_ISL_201920	North America	United States
A/Michigan/68/2015	EPI_ISL_202773	North America	United States
A/Minnesota/03/2011	EPI_ISL_88111	North America	United States
A/Minnesota/18/2017	EPI_ISL_259826	North America	United States
A/Minnesota/23/2018	EPI_ISL_306794	North America	United States
A/Minnesota/25/2017	EPI_ISL_262721	North America	United States
A/Minnesota/35/2018	EPI_ISL_312972	North America	United States
A/Minnesota/40/2009	EPI_ISL_71400	North America	United States
A/Minnesota/56/2015	EPI_ISL_213205	North America	United States
A/Mississippi/01/2009	EPI_ISL_60811	North America	United States
A/Mississippi/09/2013	EPI_ISL_154812	North America	United States
A/Mississippi/10/2013	EPI_ISL_153071	North America	United States
A/Mississippi/11/2013	EPI_ISL_151839	North America	United States
A/Mississippi/27/2017	EPI_ISL_284848	North America	United States
A/Mississippi/28/2013	EPI_ISL_153091	North America	United States
A/Mississippi/29/2013	EPI_ISL_153090	North America	United States

A/Mississippi/29/2017	EPI_ISL_286075	North America	United States
A/Missouri/02/2014	EPI_ISL_159529	North America	United States
A/Nebraska/04/2016	EPI_ISL_213178	North America	United States
A/Nebraska/20/2015	EPI_ISL_207935	North America	United States
A/Nevada/01/2010	EPI_ISL_71404	North America	United States
A/Nevada/24/2013	EPI_ISL_154811	North America	United States
A/New Hampshire/04/2013	EPI_ISL_153074	North America	United States
A/New Hampshire/08/2016	EPI_ISL_221075	North America	United States
A/New Hampshire/11/2017	EPI_ISL_258148	North America	United States
A/New Hampshire/17/2016	EPI_ISL_222212	North America	United States
A/New Hampshire/43/2015	EPI_ISL_207372	North America	United States
A/New Mexico/04/2009	EPI_ISL_30096	North America	United States
A/New Mexico/04/2011	EPI_ISL_90942	North America	United States
A/New Mexico/05/2011	EPI_ISL_90943	North America	United States
A/New Mexico/06/2011	EPI_ISL_90944	North America	United States
A/New Mexico/31/2015	EPI_ISL_215066	North America	United States
A/New York/03/2010	EPI_ISL_73409	North America	United States
A/New York/0357/2009	EPI_ISL_74125	North America	United States
A/New York/05/2018	EPI_ISL_300011	North America	United States
A/New York/14/2010	EPI_ISL_90949	North America	United States
A/New York/15/2016	EPI_ISL_214215	North America	United States
A/New York/1669/2009	EPI_ISL_60935	North America	United States
A/New York/1680/2010	EPI_ISL_74127	North America	United States
A/New York/1998/2010	EPI_ISL_74129	North America	United States
A/New York/1999/2010	EPI_ISL_74130	North America	United States
A/New York/2175/2010	EPI_ISL_74131	North America	United States
A/New York/2372/2010	EPI_ISL_74132	North America	United States
A/New York/2648/2010	EPI_ISL_74134	North America	United States
A/New York/2960/2010	EPI_ISL_74136	North America	United States
A/New York/2963/2010	EPI_ISL_74137	North America	United States
A/New York/2971/2010	EPI_ISL_74138	North America	United States
A/New York/3236/2010	EPI_ISL_74140	North America	United States
A/New York/3250/2010	EPI_ISL_74141	North America	United States
A/New York/3262/2009	EPI_ISL_30479	North America	United States
A/New York/34/2012	EPI_ISL_128404	North America	United States
A/New York/3567/2009	EPI_ISL_33868	North America	United States
A/New York/3681/2010	EPI_ISL_76231	North America	United States
A/New York/3834/2010	EPI_ISL_76234	North America	United States
A/New York/3967/2009	EPI_ISL_61329	North America	United States

A/New York/41/2014	EPI_ISL_173275	North America	United States
A/New York/4944/2009	EPI_ISL_71239	North America	United States
A/New York/4977/2009	EPI_ISL_70762	North America	United States
A/New York/5276/2009	EPI_ISL_71492	North America	United States
A/New York/6182/2009	EPI_ISL_71271	North America	United States
A/New York/6571/2009	EPI_ISL_71281	North America	United States
A/New York/6668/2009	EPI_ISL_71284	North America	United States
A/New York/74/2015	EPI_ISL_210334	North America	United States
A/New York/7420/2010	EPI_ISL_76240	North America	United States
A/North Carolina/02/2011	EPI_ISL_88124	North America	United States
A/North Carolina/04/2014	EPI_ISL_166344	North America	United States
A/North Carolina/05/2010	EPI_ISL_71958	North America	United States
A/North Carolina/06/2011	EPI_ISL_89907	North America	United States
A/North Carolina/07/2011	EPI_ISL_89908	North America	United States
A/North Carolina/08/2011	EPI_ISL_89909	North America	United States
A/North Carolina/09/2011	EPI_ISL_89910	North America	United States
A/North Carolina/09/2012	EPI_ISL_117047	North America	United States
A/North Carolina/18/2012	EPI_ISL_121448	North America	United States
A/North Carolina/43/2018	EPI_ISL_336787	North America	United States
A/North Dakota/05/2016	EPI_ISL_214195	North America	United States
A/North Dakota/21/2016	EPI_ISL_216127	North America	United States
A/North Dakota/24/2016	EPI_ISL_221224	North America	United States
A/Ohio/18/2016	EPI_ISL_227527	North America	United States
A/Oklahoma/12/2016	EPI_ISL_240284	North America	United States
A/Ontario/RV4208/2018	EPI_ISL_338699	North America	Canada
A/Pennsylvania/01/2014	EPI_ISL_157857	North America	United States
A/Pennsylvania/02/2011	EPI_ISL_88135	North America	United States
A/Pennsylvania/04/2014	EPI_ISL_157858	North America	United States
A/Pennsylvania/05/2014	EPI_ISL_157860	North America	United States
A/Pennsylvania/07/2011	EPI_ISL_90951	North America	United States
A/Pennsylvania/07/2013	EPI_ISL_156812	North America	United States
A/Pennsylvania/08/2011	EPI_ISL_90952	North America	United States
A/Pennsylvania/14/2014	EPI_ISL_159669	North America	United States
A/Pennsylvania/15/2014	EPI_ISL_159350	North America	United States
A/Pennsylvania/17/2010	EPI_ISL_84181	North America	United States
A/Pennsylvania/17/2014	EPI_ISL_159530	North America	United States
A/Pennsylvania/18/2014	EPI_ISL_159345	North America	United States
A/Pennsylvania/19/2014	EPI_ISL_159348	North America	United States
A/Pennsylvania/20/2014	EPI_ISL_159668	North America	United States

A/Pennsylvania/21/2014	EPI_ISL_159532	North America	United States
A/Pennsylvania/311/2018	EPI_ISL_361754	North America	United States
A/Pennsylvania/326/2017	EPI_ISL_295882	North America	United States
A/Pennsylvania/48/2015	EPI_ISL_205492	North America	United States
A/Pennsylvania/536/2018	EPI_ISL_358729	North America	United States
A/Pennsylvania/98/2018	EPI_ISL_358524	North America	United States
A/Pensacola/INS211/2009	EPI_ISL_76903	North America	United States
A/Puerto Rico/01/2013	EPI_ISL_145509	North America	Puerto Rico
A/Puerto Rico/29/2014	EPI_ISL_175253	North America	Puerto Rico
A/Puerto Rico/31/2014	EPI_ISL_175255	North America	Puerto Rico
A/Puerto Rico/32/2014	EPI_ISL_175257	North America	Puerto Rico
A/Puerto Rico/34/2014	EPI_ISL_175256	North America	Puerto Rico
A/Puerto Rico/48/2015	EPI_ISL_208491	North America	Puerto Rico
A/Rhode Island/09/2013	EPI_ISL_155031	North America	United States
A/Rhode Island/09/2017	EPI_ISL_258149	North America	United States
A/Rhode Island/19/2016	EPI_ISL_221094	North America	United States
A/South Dakota/10/2016	EPI_ISL_218091	North America	United States
A/South Dakota/14/2016	EPI_ISL_221649	North America	United States
A/South Dakota/14/2017	EPI_ISL_257815	North America	United States
A/South Dakota/18/2016	EPI_ISL_221653	North America	United States
A/South Dakota/41/2015	EPI_ISL_210339	North America	United States
A/Tennessee/01/2010	EPI_ISL_71422	North America	United States
A/Tennessee/31/2016	EPI_ISL_264367	North America	United States
A/Texas/09/2011	EPI_ISL_89923	North America	United States
A/Texas/09/2014	EPI_ISL_156765	North America	United States
A/Texas/100/2018	EPI_ISL_358497	North America	United States
A/Texas/101/2017	EPI_ISL_266682	North America	United States
A/Texas/102/2016	EPI_ISL_224172	North America	United States
A/Texas/146/2016	EPI_ISL_232626	North America	United States
A/Texas/22/2012	EPI_ISL_111395	North America	United States
A/Texas/23/2012	EPI_ISL_115085	North America	United States
A/Texas/26/2012	EPI_ISL_117346	North America	United States
A/Texas/27/2012	EPI_ISL_118689	North America	United States
A/Texas/323/2017	EPI_ISL_292658	North America	United States
A/Texas/418/2017	EPI_ISL_358504	North America	United States
A/Texas/46240925/2009	EPI_ISL_73495	North America	United States
A/Texas/79/2015	EPI_ISL_227425	North America	United States
A/Trinidad/429/2015	EPI_ISL_193602	North America	Trinidad and Tobago
A/Utah/02/2010	EPI_ISL_71432	North America	United States

A/Utah/03/2010	EPI_ISL_73411	North America	United States
A/Utah/10/2013	EPI_ISL_150613	North America	United States
A/Utah/15/2016	EPI_ISL_218086	North America	United States
A/Utah/19/2016	EPI_ISL_218114	North America	United States
A/Utah/32/2017	EPI_ISL_284069	North America	United States
A/Utah/45/2017	EPI_ISL_295900	North America	United States
A/Vermont/16/2018	EPI_ISL_309492	North America	United States
A/Virginia/01/2010	EPI_ISL_71435	North America	United States
A/Virginia/04/2011	EPI_ISL_88151	North America	United States
A/Virginia/06/2014	EPI_ISL_159349	North America	United States
A/Virginia/40/2014	EPI_ISL_172643	North America	United States
A/Virginia/51/2016	EPI_ISL_223305	North America	United States
A/Virginia/59/2016	EPI_ISL_230541	North America	United States
A/Washington/02/2011	EPI_ISL_88152	North America	United States
A/Washington/07/2014	EPI_ISL_159391	North America	United States
A/Washington/10/2017	EPI_ISL_248964	North America	United States
A/Washington/166/2018	EPI_ISL_360927	North America	United States
A/Washington/19/2015	EPI_ISL_178490	North America	United States
A/Washington/24/2012	EPI_ISL_134841	North America	United States
A/Washington/299/2017	EPI_ISL_284071	North America	United States
A/Washington/59/2014	EPI_ISL_173267	North America	United States
A/West Virginia/27/2018	EPI_ISL_312931	North America	United States
A/Wisconsin/01/2010	EPI_ISL_71444	North America	United States
A/Wisconsin/101/2016	EPI_ISL_241645	North America	United States
A/Wisconsin/110/2018	EPI_ISL_361178	North America	United States
A/Wisconsin/15/2011	EPI_ISL_89930	North America	United States
A/Wisconsin/16/2011	EPI_ISL_89931	North America	United States
A/Wisconsin/18/2011	EPI_ISL_89933	North America	United States
A/Wisconsin/187/2018	EPI_ISL_361250	North America	United States
A/Wisconsin/25/2015	EPI_ISL_178491	North America	United States
A/Wisconsin/354/2017	EPI_ISL_296032	North America	United States
A/Wisconsin/42/2017	EPI_ISL_259840	North America	United States
A/Wisconsin/45/2017	EPI_ISL_261838	North America	United States
A/Wisconsin/496/2018	EPI_ISL_331159	North America	United States
A/Wisconsin/629 D00015/2009	EPI_ISL_61530	North America	United States
A/Wisconsin/629 D00349/2009	EPI_ISL_61539	North America	United States
A/Wisconsin/629 D00672/2009	EPI_ISL_71526	North America	United States
A/Wisconsin/629 D01015/2009	EPI_ISL_71717	North America	United States
A/Wisconsin/629 D01083/2009	EPI_ISL_61566	North America	United States

A/Wisconsin/629 D01412/2009	EPI_ISL_71552	North America	United States
A/Wisconsin/629 D01705/2009	EPI_ISL_61585	North America	United States
A/Wisconsin/629 D01903/2009	EPI_ISL_62670	North America	United States
A/Wisconsin/629 D02272/2009	EPI_ISL_61610	North America	United States
A/Wisconsin/629 S1350/2009	EPI_ISL_71583	North America	United States
A/Wisconsin/88/2015	EPI_ISL_207386	North America	United States
A/Wisconsin/90/2015	EPI_ISL_207379	North America	United States
A/Wyoming/04/2018	EPI_ISL_299998	North America	United States
A/Acre/140837-IEC/2016	EPI_ISL_233546	South America	Brazil
A/Acre/152954-IEC/2018	EPI_ISL_320216	South America	Brazil
A/Amapa/141547-IEC/2016	EPI_ISL_233552	South America	Brazil
A/Amazonas/141200-IEC/2016	EPI_ISL_233548	South America	Brazil
A/Antofagasta/37835/2018	EPI_ISL_320709	South America	Chile
A/Argentina/07-09GP/2009	EPI_ISL_76251	South America	Argentina
A/Argentina/08AR/2009	EPI_ISL_76253	South America	Argentina
A/Argentina/115/2015	EPI_ISL_197806	South America	Argentina
A/Argentina/11551/2015	EPI_ISL_200997	South America	Argentina
A/Argentina/12776/2017	EPI_ISL_281611	South America	Argentina
A/Argentina/12777/2017	EPI_ISL_281610	South America	Argentina
A/Argentina/12780/2017	EPI_ISL_281612	South America	Argentina
A/Argentina/13743/2018	EPI_ISL_329905	South America	Argentina
A/Argentina/19527/2009	EPI_ISL_76255	South America	Argentina
A/Argentina/19618/2009	EPI_ISL_76257	South America	Argentina
A/Argentina/19656/2009	EPI_ISL_76258	South America	Argentina
A/Argentina/22/2015	EPI_ISL_197805	South America	Argentina
A/Argentina/262/2015	EPI_ISL_197811	South America	Argentina
A/Argentina/269/2018	EPI_ISL_322902	South America	Argentina
A/Argentina/36/2015	EPI_ISL_197809	South America	Argentina
A/Argentina/610/2016	EPI_ISL_227500	South America	Argentina
A/Argentina/720/2016	EPI_ISL_230495	South America	Argentina
A/Argentina/7768/2009	EPI_ISL_34542	South America	Argentina
A/Argentina/8169/2009	EPI_ISL_71348	South America	Argentina
A/Argentina/92/2015	EPI_ISL_197812	South America	Argentina
A/Argentina/HNRG13/2009	EPI_ISL_66020	South America	Argentina
A/Argentina/HNRG3/2009	EPI_ISL_66029	South America	Argentina
A/Argentina/HNRG32/2009	EPI_ISL_66032	South America	Argentina
A/Argentina/HNRG45/2009	EPI_ISL_66041	South America	Argentina
A/Bahia/133/2017	EPI_ISL_268463	South America	Brazil
A/Bogota/0466N/2009	EPI_ISL_33946	South America	Colombia

A/Bogota/WR0090N/2009	EPI_ISL_61785	South America	Colombia
A/Bolivia/0883/2018	EPI_ISL_329904	South America	Bolivia
A/Bolivia/1696/2018	EPI_ISL_333041	South America	Bolivia
A/Bolivia/171/2018	EPI_ISL_332206	South America	Bolivia
A/Bolivia/1723/2018	EPI_ISL_322915	South America	Bolivia
A/Bolivia/1838/2018	EPI_ISL_330876	South America	Bolivia
A/Bolivia/2127/2016	EPI_ISL_239229	South America	Bolivia
A/Bolivia/2324/2018	EPI_ISL_322894	South America	Bolivia
A/Bolivia/3327/2018	EPI_ISL_333050	South America	Bolivia
A/Bolivia/3454/2018	EPI_ISL_333056	South America	Bolivia
A/Bolivia/3469/2018	EPI_ISL_333057	South America	Bolivia
A/Bolivia/351/2017	EPI_ISL_269953	South America	Bolivia
A/Bolivia/493/2017	EPI_ISL_273783	South America	Bolivia
A/Bolivia/510/2017	EPI_ISL_273794	South America	Bolivia
A/Bolivia/559/2013	EPI_ISL_145507	South America	Bolivia
A/Bolivia/586/2017	EPI_ISL_273793	South America	Bolivia
A/Bolivia/608/2017	EPI_ISL_273785	South America	Bolivia
A/Bolivia/638/2017	EPI_ISL_273786	South America	Bolivia
A/Bolivia/714/2017	EPI_ISL_273787	South America	Bolivia
A/Bolivia/750/2017	EPI_ISL_273788	South America	Bolivia
A/Bolivia/792/2017	EPI_ISL_273784	South America	Bolivia
A/Bolivia/800/2017	EPI_ISL_273789	South America	Bolivia
A/Brazil/0257 S2/2016	EPI_ISL_233535	South America	Brazil
A/Brazil/0480/2016	EPI_ISL_233053	South America	Brazil
A/Brazil/0504/2015	EPI_ISL_213115	South America	Brazil
A/Brazil/0638/2015	EPI_ISL_214164	South America	Brazil
A/Brazil/1170/2016	EPI_ISL_235329	South America	Brazil
A/Brazil/126/2015	EPI_ISL_223344	South America	Brazil
A/Brazil/1335/2016	EPI_ISL_223209	South America	Brazil
A/Brazil/1456/2018	EPI_ISL_330410	South America	Brazil
A/Brazil/1923/2016	EPI_ISL_277209	South America	Brazil
A/Brazil/193/2016	EPI_ISL_227466	South America	Brazil
A/Brazil/2391/2018	EPI_ISL_321957	South America	Brazil
A/Brazil/2817/2018	EPI_ISL_319841	South America	Brazil
A/Brazil/3032/2016	EPI_ISL_223214	South America	Brazil
A/Brazil/3169/2018	EPI_ISL_316749	South America	Brazil
A/Brazil/40863/2016	EPI_ISL_237820	South America	Brazil
A/Brazil/5026/2017	EPI_ISL_281608	South America	Brazil
A/Brazil/5243/2016	EPI_ISL_233592	South America	Brazil

A/Brazil/526/2017	EPI_ISL_275660	South America	Brazil
A/Brazil/536/2017	EPI_ISL_275661	South America	Brazil
A/Brazil/5662/2016	EPI_ISL_244226	South America	Brazil
A/Brazil/69221/2015	EPI_ISL_207377	South America	Brazil
A/Brazil/72880/2015	EPI_ISL_206984	South America	Brazil
A/Brazil/764/2009	EPI_ISL_35003	South America	Brazil
A/Brazil/8253/2018	EPI_ISL_333062	South America	Brazil
A/Ceara/145605-IEC/2017	EPI_ISL_275655	South America	Brazil
A/Chile/1579/2009	EPI_ISL_64985	South America	Chile
A/Chile/6536/2009	EPI_ISL_60789	South America	Chile
A/Chile/8945/2009	EPI_ISL_33573	South America	Chile
A/Chile/8949/2009	EPI_ISL_33574	South America	Chile
A/Colombia/0103/2018	EPI_ISL_322917	South America	Colombia
A/Colombia/0137/2016	EPI_ISL_234624	South America	Colombia
A/Colombia/0559/2018	EPI_ISL_322906	South America	Colombia
A/Colombia/1359/2015	EPI_ISL_190443	South America	Colombia
A/Colombia/1457/2015	EPI_ISL_190445	South America	Colombia
A/Colombia/2537/2015	EPI_ISL_190446	South America	Colombia
A/Colombia/3732/2017	EPI_ISL_273762	South America	Colombia
A/Colombia/4280/2015	EPI_ISL_178103	South America	Colombia
A/Colombia/4522/2015	EPI_ISL_190442	South America	Colombia
A/Colombia/4790/2017	EPI_ISL_277622	South America	Colombia
A/Colombia/497/2015	EPI_ISL_215025	South America	Colombia
A/Colombia/6863/2015	EPI_ISL_215027	South America	Colombia
A/Colombia/7242/2016	EPI_ISL_215028	South America	Colombia
A/Colombia/8237/2018	EPI_ISL_312916	South America	Colombia
A/Colombia/9833/2018	EPI_ISL_322918	South America	Colombia
A/Colombia/9953/2016	EPI_ISL_241735	South America	Colombia
A/Concepcion/39745/2015	EPI_ISL_200782	South America	Chile
A/Concepcion/39751/2015	EPI_ISL_200777	South America	Chile
A/Concepcion/44321/2015	EPI_ISL_194846	South America	Chile
A/Ecuador/1155/2018	EPI_ISL_320242	South America	Ecuador
A/Ecuador/14/2018	EPI_ISL_300087	South America	Ecuador
A/Ecuador/222/2017	EPI_ISL_273797	South America	Ecuador
A/Ecuador/2375/2015	EPI_ISL_194930	South America	Ecuador
A/Ecuador/2495/2017	EPI_ISL_299993	South America	Ecuador
A/Ecuador/33/2017	EPI_ISL_273796	South America	Ecuador
A/Ecuador/330/2016	EPI_ISL_233035	South America	Ecuador
A/Ecuador/3670/2017	EPI_ISL_300082	South America	Ecuador

A/Ecuador/3904/2018	EPI_ISL_320245	South America	Ecuador
A/Ecuador/533/2017	EPI_ISL_300083	South America	Ecuador
A/Ecuador/609/2017	EPI_ISL_299996	South America	Ecuador
A/Ecuador/625/2017	EPI_ISL_300078	South America	Ecuador
A/Ecuador/72/2018	EPI_ISL_300085	South America	Ecuador
A/Ecuador/731/2017	EPI_ISL_299997	South America	Ecuador
A/Ecuador/98/2016	EPI_ISL_233039	South America	Ecuador
A/Ecuador/997/2017	EPI_ISL_302838	South America	Ecuador
A/French Guiana/4072/2015	EPI_ISL_195795	South America	French Guiana
A/French Guiana/6135/2015	EPI_ISL_197566	South America	French Guiana
A/Guyane/341/2017	EPI_ISL_303162	South America	French Guiana
A/Guyane/354/2017	EPI_ISL_304294	South America	French Guiana
A/Guyane/355/2017	EPI_ISL_300892	South America	French Guiana
A/Guyane/622/2018	EPI_ISL_321285	South America	French Guiana
A/La Paz/WR0096T/2009	EPI_ISL_61807	South America	Bolivia
A/Para/139207-IEC/2016	EPI_ISL_233543	South America	Brazil
A/Para/140720-IEC/2016	EPI_ISL_233544	South America	Brazil
A/Paraguay/0021/2016	EPI_ISL_232129	South America	Paraguay
A/Paraguay/0778/2016	EPI_ISL_232693	South America	Paraguay
A/Paraguay/1164/2015	EPI_ISL_195825	South America	Paraguay
A/Paraguay/3792/2016	EPI_ISL_232695	South America	Paraguay
A/Paraguay/5333/2015	EPI_ISL_195822	South America	Paraguay
A/Paraguay/5487/2015	EPI_ISL_195824	South America	Paraguay
A/Paraguay/6987/2015	EPI_ISL_210336	South America	Paraguay
A/Paraguay/7466/2015	EPI_ISL_210337	South America	Paraguay
A/Paraguay/7481/2015	EPI_ISL_210338	South America	Paraguay
A/Paraiba/143594-IEC/2016	EPI_ISL_248207	South America	Brazil
A/Paraiba/152186-IEC/2018	EPI_ISL_320229	South America	Brazil
A/Pernambuco/138995-IEC/2016	EPI_ISL_233563	South America	Brazil
A/Peru/06/2015	EPI_ISL_192548	South America	Peru
A/Peru/0716/2016	EPI_ISL_238786	South America	Peru
A/Peru/08/2015	EPI_ISL_192643	South America	Peru
A/Peru/10/2015	EPI_ISL_192640	South America	Peru
A/Peru/106/2013	EPI_ISL_143679	South America	Peru
A/Peru/11/2015	EPI_ISL_192642	South America	Peru
A/Peru/18/2015	EPI_ISL_192641	South America	Peru
A/Peru/2093/2015	EPI_ISL_203292	South America	Peru
A/Peru/45918/2018	EPI_ISL_321972	South America	Peru
A/Peru/48/2016	EPI_ISL_230526	South America	Peru

A/Peru/51/2015	EPI_ISL_203613	South America	Peru
A/Peru/52/2016	EPI_ISL_232685	South America	Peru
A/Peru/55/2016	EPI_ISL_232155	South America	Peru
A/Peru/56/2016	EPI_ISL_232156	South America	Peru
A/Peru/63/2015	EPI_ISL_202369	South America	Peru
A/Peru/67118/2018	EPI_ISL_321962	South America	Peru
A/Peru/8409/2009	EPI_ISL_70317	South America	Peru
A/Peru/9118/2018	EPI_ISL_319808	South America	Peru
A/Peru/9318/2018	EPI_ISL_319825	South America	Peru
A/Peru/9818/2018	EPI_ISL_319810	South America	Peru
A/Pucon/73761/2015	EPI_ISL_213112	South America	Chile
A/Puerto Montt/51370/2016	EPI_ISL_233031	South America	Chile
A/Quillota/25269/2016	EPI_ISL_227479	South America	Chile
A/Quito/WR1589N/2009	EPI_ISL_78833	South America	Ecuador
A/Rio Grande Do Norte/141183/2016	EPI_ISL_233547	South America	Brazil
A/Rio Grande Do Sul/17/2017	EPI_ISL_268414	South America	Brazil
A/Roraima/143204-IEC/2017	EPI_ISL_248206	South America	Brazil
A/Santa Catarina/92/2017	EPI_ISL_275631	South America	Brazil
A/Santiago/33499/2018	EPI_ISL_314546	South America	Chile
A/Santiago/45801/2016	EPI_ISL_232734	South America	Chile
A/Santiago/78647/2018	EPI_ISL_347489	South America	Chile
A/Suriname/0167/2018	EPI_ISL_330849	South America	Suriname
A/Suriname/0777/2010	EPI_ISL_73793	South America	Suriname
A/Suriname/1437/2016	EPI_ISL_253047	South America	Suriname
A/Suriname/2158/2017	EPI_ISL_275662	South America	Suriname
A/Uruguay/597/2018	EPI_ISL_330180	South America	Uruguay
A/Uruguay/755/2009	EPI_ISL_35025	South America	Uruguay
A/Valparaiso/25941/2016	EPI_ISL_227480	South America	Chile
A/Valparaiso/27731/2016	EPI_ISL_227481	South America	Chile
A/Valparaiso/68954/2015	EPI_ISL_214162	South America	Chile
A/Venezuela/01/2018	EPI_ISL_321946	South America	Venezuela
A/Venezuela/10/2018	EPI_ISL_321945	South America	Venezuela
A/Venezuela/30/2018	EPI_ISL_348094	South America	Venezuela
A/AUCKLAND/64/2012	EPI_ISL_134453	Oceania	New Zealand
A/AUCKLAND/8/2014	EPI_ISL_168841	Oceania	New Zealand
A/Australia/11/2009	EPI_ISL_70674	Oceania	Australia
A/Australia/12/2009	EPI_ISL_70675	Oceania	Australia
A/Australia/16/2009	EPI_ISL_70679	Oceania	Australia
A/Australia/21/2009	EPI_ISL_70681	Oceania	Australia

A/Australia/23/2009	EPI_ISL_70682	Oceania	Australia
A/Australia/24/2009	EPI_ISL_70684	Oceania	Australia
A/Australia/25/2009	EPI_ISL_70685	Oceania	Australia
A/Australia/26/2009	EPI_ISL_70686	Oceania	Australia
A/Australia/28/2009	EPI_ISL_70688	Oceania	Australia
A/Australia/40/2009	EPI_ISL_70696	Oceania	Australia
A/Australia/42/2009	EPI_ISL_70697	Oceania	Australia
A/Australia/43/2009	EPI_ISL_70698	Oceania	Australia
A/Australia/54/2009	EPI_ISL_70705	Oceania	Australia
A/Australia/56/2009	EPI_ISL_70706	Oceania	Australia
A/Australia/57/2009	EPI_ISL_70707	Oceania	Australia
A/Australia/58/2009	EPI_ISL_70708	Oceania	Australia
A/Australia/59/2009	EPI_ISL_70709	Oceania	Australia
A/Australia/6/2009	EPI_ISL_68089	Oceania	Australia
A/Australia/61/2009	EPI_ISL_70711	Oceania	Australia
A/Australia/63/2009	EPI_ISL_70712	Oceania	Australia
A/Australia/64/2009	EPI_ISL_70713	Oceania	Australia
A/Australia/69/2009	EPI_ISL_70716	Oceania	Australia
A/Australia/70/2009	EPI_ISL_70718	Oceania	Australia
A/Australia/82/2009	EPI_ISL_70724	Oceania	Australia
A/Brisbane/02/2018	EPI_ISL_330190	Oceania	Australia
A/BRISBANE/1007/2014	EPI_ISL_168953	Oceania	Australia
A/Brisbane/1018/2018	EPI_ISL_332774	Oceania	Australia
A/Brisbane/103/2016	EPI_ISL_227599	Oceania	Australia
A/Brisbane/137/2015	EPI_ISL_219024	Oceania	Australia
A/Brisbane/151/2018	EPI_ISL_338257	Oceania	Australia
A/Brisbane/159/2018	EPI_ISL_338254	Oceania	Australia
A/Brisbane/200/2017	EPI_ISL_312596	Oceania	Australia
A/BRISBANE/210/2011	EPI_ISL_101516	Oceania	Australia
A/Brisbane/28/2013	EPI_ISL_172856	Oceania	Australia
A/Brisbane/294/2016	EPI_ISL_243993	Oceania	Australia
A/Brisbane/305/2016	EPI_ISL_246667	Oceania	Australia
A/Brisbane/35/2015	EPI_ISL_195823	Oceania	Australia
A/Brisbane/37/2017	EPI_ISL_269278	Oceania	Australia
A/BRISBANE/6/2013	EPI_ISL_141542	Oceania	Australia
A/Brisbane/70/2011	EPI_ISL_100105	Oceania	Australia
A/Brisbane/78/2018	EPI_ISL_320947	Oceania	Australia
A/Canberra/1/2016	EPI_ISL_222773	Oceania	Australia
A/Canberra/1014/2017	EPI_ISL_312590	Oceania	Australia

A/Canterbury/25/2017	EPI_ISL_312589	Oceania	New Zealand
A/CHRISTCHURCH/18/2011	EPI_ISL_101547	Oceania	New Zealand
A/CHRISTCHURCH/538/2014	EPI_ISL_168850	Oceania	New Zealand
A/CHRISTCHURCH/60/2011	EPI_ISL_106845	Oceania	New Zealand
A/DARWIN/104/2013	EPI_ISL_161865	Oceania	Australia
A/Darwin/118/2018	EPI_ISL_338245	Oceania	Australia
A/Darwin/122/2018	EPI_ISL_333978	Oceania	Australia
A/Darwin/123/2018	EPI_ISL_391378	Oceania	Australia
A/Darwin/21/2018	EPI_ISL_333986	Oceania	Australia
A/Darwin/25/2018	EPI_ISL_333989	Oceania	Australia
A/Darwin/35/2018	EPI_ISL_333993	Oceania	Australia
A/Darwin/37/2018	EPI_ISL_333995	Oceania	Australia
A/Darwin/4/2018	EPI_ISL_338264	Oceania	Australia
A/Darwin/47/2018	EPI_ISL_334066	Oceania	Australia
A/Darwin/5/2018	EPI_ISL_338263	Oceania	Australia
A/Darwin/50/2018	EPI_ISL_333999	Oceania	Australia
A/Darwin/51/2018	EPI_ISL_334000	Oceania	Australia
A/Darwin/52/2018	EPI_ISL_334001	Oceania	Australia
A/Darwin/55/2018	EPI_ISL_334071	Oceania	Australia
A/DARWIN/56/2013	EPI_ISL_148746	Oceania	Australia
A/Darwin/6/2018	EPI_ISL_349822	Oceania	Australia
A/Darwin/67/2018	EPI_ISL_334072	Oceania	Australia
A/Darwin/69/2018	EPI_ISL_334074	Oceania	Australia
A/Darwin/74/2018	EPI_ISL_334076	Oceania	Australia
A/Darwin/80/2018	EPI_ISL_334008	Oceania	Australia
A/Darwin/86/2018	EPI_ISL_338258	Oceania	Australia
A/Darwin/91/2018	EPI_ISL_338260	Oceania	Australia
A/Darwin/95/2018	EPI_ISL_338261	Oceania	Australia
A/Dunedin/4/2017	EPI_ISL_312588	Oceania	New Zealand
A/Dunedin/9/2016	EPI_ISL_237875	Oceania	New Zealand
A/Fiji/2/2016	EPI_ISL_227596	Oceania	Fiji
A/FIJI/4/2012	EPI_ISL_128688	Oceania	Fiji
A/Fiji/63/2016	EPI_ISL_255507	Oceania	Fiji
A/Fiji/8/2016	EPI_ISL_227598	Oceania	Fiji
A/Gisborne/1/2016	EPI_ISL_243923	Oceania	New Zealand
A/GOROKA/27/2013	EPI_ISL_151482	Oceania	Papua New Guinea
A/Guam/NHRC0001/2009	EPI_ISL_76450	Oceania	Guam
A/Guam/NHRC0004/2009	EPI_ISL_77854	Oceania	Guam
A/Guam/NHRC0006/2009	EPI_ISL_78762	Oceania	Guam

A/Guam/NHRC0009/2009	EPI_ISL_77857	Oceania	Guam
A/Guam/NHRC0011/2009	EPI_ISL_77859	Oceania	Guam
A/Guam/NHRC0016/2009	EPI_ISL_77864	Oceania	Guam
A/Guam/NHRC0018/2009	EPI_ISL_77866	Oceania	Guam
A/Guam/NHRC0020/2009	EPI_ISL_77868	Oceania	Guam
A/Guam/NHRC0023/2009	EPI_ISL_77871	Oceania	Guam
A/Guam/NHRC0024/2009	EPI_ISL_77872	Oceania	Guam
A/Guam/NHRC0025/2009	EPI_ISL_77873	Oceania	Guam
A/Guam/NHRC0029/2009	EPI_ISL_78764	Oceania	Guam
A/Guam/NHRC0030/2009	EPI_ISL_78765	Oceania	Guam
A/Guam/NHRC0031/2009	EPI_ISL_78766	Oceania	Guam
A/Guam/NHRC0032/2009	EPI_ISL_78767	Oceania	Guam
A/New Caledonia/14/2018	EPI_ISL_346463	Oceania	New Caledonia
A/NEW CALEDONIA/58/2013	EPI_ISL_161860	Oceania	New Caledonia
A/NEW CALEDONIA/58/2014	EPI_ISL_166169	Oceania	New Caledonia
A/NEW CALEDONIA/72/2014	EPI_ISL_168854	Oceania	New Caledonia
A/New Zealand/0815/2016	EPI_ISL_240215	Oceania	New Zealand
A/New Zealand/0841/2016	EPI_ISL_235322	Oceania	New Zealand
A/New Zealand/0842/2016	EPI_ISL_240217	Oceania	New Zealand
A/New Zealand/0967/2016	EPI_ISL_240219	Oceania	New Zealand
A/New Zealand/1057/2017	EPI_ISL_284821	Oceania	New Zealand
A/New Zealand/1076/2017	EPI_ISL_284823	Oceania	New Zealand
A/New Zealand/1148/2016	EPI_ISL_241696	Oceania	New Zealand
A/New Zealand/1150/2016	EPI_ISL_240223	Oceania	New Zealand
A/New Zealand/1258/2017	EPI_ISL_285770	Oceania	New Zealand
A/New Zealand/1417/2017	EPI_ISL_284820	Oceania	New Zealand
A/New Zealand/1483/2017	EPI_ISL_284819	Oceania	New Zealand
A/New Zealand/1566/2017	EPI_ISL_284818	Oceania	New Zealand
A/New Zealand/1755/2017	EPI_ISL_284817	Oceania	New Zealand
A/New Zealand/1898/2017	EPI_ISL_284834	Oceania	New Zealand
A/New Zealand/1937/2016	EPI_ISL_235323	Oceania	New Zealand
A/New Zealand/1949/2017	EPI_ISL_285763	Oceania	New Zealand
A/New Zealand/2021/2017	EPI_ISL_284816	Oceania	New Zealand
A/New Zealand/2023/2017	EPI_ISL_284815	Oceania	New Zealand
A/New Zealand/2044/2017	EPI_ISL_286086	Oceania	New Zealand
A/New Zealand/2183/2017	EPI_ISL_284830	Oceania	New Zealand
A/New Zealand/219/2017	EPI_ISL_275651	Oceania	New Zealand
A/New Zealand/2264/2017	EPI_ISL_284829	Oceania	New Zealand
A/New Zealand/2280/2017	EPI_ISL_284828	Oceania	New Zealand

A/New Zealand/2287/2017	EPI_ISL_286073	Oceania	New Zealand
A/New Zealand/2309/2017	EPI_ISL_284827	Oceania	New Zealand
A/New Zealand/2333/2017	EPI_ISL_286071	Oceania	New Zealand
A/New Zealand/2341/2017	EPI_ISL_286087	Oceania	New Zealand
A/New Zealand/2388/2017	EPI_ISL_286085	Oceania	New Zealand
A/New Zealand/2395/2017	EPI_ISL_286083	Oceania	New Zealand
A/New Zealand/245/2017	EPI_ISL_275652	Oceania	New Zealand
A/New Zealand/476/2017	EPI_ISL_275653	Oceania	New Zealand
A/New Zealand/551/2017	EPI_ISL_284825	Oceania	New Zealand
A/New Zealand/591/2017	EPI_ISL_275654	Oceania	New Zealand
A/New Zealand/871/2009	EPI_ISL_73420	Oceania	New Zealand
A/New Zealand/963/2017	EPI_ISL_284824	Oceania	New Zealand
A/New Zealand/971/2017	EPI_ISL_285773	Oceania	New Zealand
A/Newcastle/106/2016	EPI_ISL_237854	Oceania	Australia
A/NEWCASTLE/163/2011	EPI_ISL_95604	Oceania	Australia
A/NEWCASTLE/17/2011	EPI_ISL_95595	Oceania	Australia
A/NEWCASTLE/170/2011	EPI_ISL_101541	Oceania	Australia
A/NEWCASTLE/179/2011	EPI_ISL_101564	Oceania	Australia
A/NEWCASTLE/58/2011	EPI_ISL_95252	Oceania	Australia
A/Newcastle/76/2018	EPI_ISL_339049	Oceania	Australia
A/Newcastle/77/2018	EPI_ISL_336002	Oceania	Australia
A/Newcastle/78/2018	EPI_ISL_339050	Oceania	Australia
A/NEWCASTLE/85/2011	EPI_ISL_95601	Oceania	Australia
A/NORTHLAND/2/2013	EPI_ISL_161309	Oceania	New Zealand
A/Papua New Guinea/29/2016	EPI_ISL_261883	Oceania	Papua New Guinea
A/Papua New Guinea/36/2016	EPI_ISL_272694	Oceania	Papua New Guinea
A/Perth/10/2017	EPI_ISL_269259	Oceania	Australia
A/PERTH/12/2010	EPI_ISL_79402	Oceania	Australia
A/PERTH/175/2011	EPI_ISL_106844	Oceania	Australia
A/Perth/183/2018	EPI_ISL_334433	Oceania	Australia
A/PERTH/194/2011	EPI_ISL_106850	Oceania	Australia
A/PERTH/298/2012	EPI_ISL_141551	Oceania	Australia
A/PERTH/299/2011	EPI_ISL_118649	Oceania	Australia
A/Perth/346/2017	EPI_ISL_312598	Oceania	Australia
A/PERTH/49/2011	EPI_ISL_101523	Oceania	Australia
A/South Auckland/2/2016	EPI_ISL_232832	Oceania	New Zealand
A/South Auckland/51/2016	EPI_ISL_237876	Oceania	New Zealand
A/South Australia/152/2018	EPI_ISL_338256	Oceania	Australia
A/SOUTH AUSTRALIA/162/2012	EPI_ISL_134468	Oceania	Australia

A/South Australia/17/2013	EPI_ISL_145643	Oceania	Australia
A/South Australia/172/2018	EPI_ISL_338252	Oceania	Australia
A/South Australia/22/2015	EPI_ISL_197576	Oceania	Australia
A/South Australia/272/2017	EPI_ISL_330191	Oceania	Australia
A/SOUTH AUSTRALIA/77/2013	EPI_ISL_151586	Oceania	Australia
A/Sydney/1006/2016	EPI_ISL_232795	Oceania	Australia
A/Sydney/15/2016	EPI_ISL_222779	Oceania	Australia
A/Sydney/231/2017	EPI_ISL_312595	Oceania	Australia
A/SYDNEY/525/2011	EPI_ISL_101556	Oceania	Australia
A/SYDNEY/56/2011	EPI_ISL_101546	Oceania	Australia
A/SYDNEY/74/2011	EPI_ISL_101566	Oceania	Australia
A/Sydney/744/2017	EPI_ISL_312592	Oceania	Australia
A/SYDNEY/82/2013	EPI_ISL_161858	Oceania	Australia
A/Tasmania/1/2016	EPI_ISL_222794	Oceania	Australia
A/Tasmania/10/2018	EPI_ISL_338251	Oceania	Australia
A/Tasmania/1042/2017	EPI_ISL_312591	Oceania	Australia
A/TASMANIA/24/2014	EPI_ISL_166026	Oceania	Australia
A/Tasmania/27/2015	EPI_ISL_194543	Oceania	Australia
A/Tasmania/32/2016	EPI_ISL_237863	Oceania	Australia
A/Tasmania/8/2017	EPI_ISL_269262	Oceania	Australia
A/Tauranga/5/2018	EPI_ISL_346467	Oceania	New Zealand
A/TOWNSVILLE/23/2013	EPI_ISL_148760	Oceania	Australia
A/Townsville/31/2016	EPI_ISL_239843	Oceania	Australia
A/TOWNSVILLE/41/2013	EPI_ISL_151501	Oceania	Australia
A/TOWNSVILLE/5/2013	EPI_ISL_148750	Oceania	Australia
A/Victoria/2102/2018	EPI_ISL_338255	Oceania	Australia
A/VICTORIA/229/2013	EPI_ISL_161332	Oceania	Australia
A/Victoria/2500/2016	EPI_ISL_272695	Oceania	Australia
A/Victoria/501/2016	EPI_ISL_236234	Oceania	Australia
A/VICTORIA/514/2012	EPI_ISL_122599	Oceania	Australia
A/Victoria/523/2012	EPI_ISL_129015	Oceania	Australia
A/Victoria/744/2018	EPI_ISL_338250	Oceania	Australia
A/Victoria/746/2018	EPI_ISL_338253	Oceania	Australia
A/VICTORIA/821/2011	EPI_ISL_101534	Oceania	Australia
A/Wellington/52/2017	EPI_ISL_312587	Oceania	New Zealand

7.3.2 Global Influenza A(H3N2) Virus Genome Details, 2010-2016

Isolate Name	GISAID Accession	Continent	Country
A/Addis Ababa/1514A07305892N/2013	EPI_ISL_235363	Africa	Ethiopia
A/Anjeva/1747/2016	EPI_ISL_233001	Africa	Madagascar
A/Antananarivo/1067/2016	EPI_ISL_281573	Africa	Madagascar
A/Antananarivo/1073/2016	EPI_ISL_230304	Africa	Madagascar
A/Antananarivo/1158/2016	EPI_ISL_230305	Africa	Madagascar
A/Antananarivo/1743/2016	EPI_ISL_232984	Africa	Madagascar
A/Antananarivo/1951/2016	EPI_ISL_230307	Africa	Madagascar
A/Antananarivo/1987/2016	EPI_ISL_230308	Africa	Madagascar
A/Antsirabe/3541/2016	EPI_ISL_239160	Africa	Madagascar
A/Antsirabe/3821/2016	EPI_ISL_239161	Africa	Madagascar
A/Antsirabe/3857/2015	EPI_ISL_206244	Africa	Madagascar
A/Burkina Faso/138/2015	EPI_ISL_220282	Africa	Burkina Faso
A/Burkina Faso/1630/2015	EPI_ISL_215614	Africa	Burkina Faso
A/Burkina Faso/1632/2015	EPI_ISL_215615	Africa	Burkina Faso
A/Burkina Faso/1633/2015	EPI_ISL_215616	Africa	Burkina Faso
A/Burkina Faso/611/2015	EPI_ISL_215617	Africa	Burkina Faso
A/Burkina Faso/613/2015	EPI_ISL_215618	Africa	Burkina Faso
A/Burkina Faso/620/2015	EPI_ISL_215770	Africa	Burkina Faso
A/Burkina Faso/640/2015	EPI_ISL_220283	Africa	Burkina Faso
A/Burkina Faso/76/2015	EPI_ISL_213975	Africa	Burkina Faso
A/Burkina Faso/87/2015	EPI_ISL_213976	Africa	Burkina Faso
A/Burkina Faso/92/2015	EPI_ISL_215619	Africa	Burkina Faso
A/Congo/0560/2016	EPI_ISL_235088	Africa	Congo
A/Congo/0938/2016	EPI_ISL_235089	Africa	Congo
A/Congo/0939/2016	EPI_ISL_235090	Africa	Congo
A/Congo/0941/2016	EPI_ISL_235091	Africa	Congo
A/Congo/0947/2016	EPI_ISL_235092	Africa	Congo
A/Congo/1137/2016	EPI_ISL_235093	Africa	Congo
A/Congo/2458/2014	EPI_ISL_175211	Africa	Congo
A/Congo/2461/2014	EPI_ISL_175217	Africa	Congo
A/Congo/2471/2014	EPI_ISL_175210	Africa	Congo
A/Congo/2495/2014	EPI_ISL_189842	Africa	Congo
A/Congo/2526/2014	EPI_ISL_191693	Africa	Congo
A/Congo/2538/2014	EPI_ISL_176513	Africa	Congo
A/Congo/2544/2014	EPI_ISL_176515	Africa	Congo
A/Congo/2557/2014	EPI_ISL_176548	Africa	Congo

A/Congo/2586/2014	EPI_ISL_191708	Africa	Congo
A/Congo/2588/2014	EPI_ISL_191672	Africa	Congo
A/Congo/2603/2014	EPI_ISL_191694	Africa	Congo
A/Congo/2611/2014	EPI_ISL_176547	Africa	Congo
A/Cote D'Ivoire/1613/2015	EPI_ISL_215628	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1616/2015	EPI_ISL_215629	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1617/2015	EPI_ISL_215630	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1638/2015	EPI_ISL_215631	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1672/2015	EPI_ISL_213977	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1916/2015	EPI_ISL_213978	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1918/2015	EPI_ISL_215632	Africa	Cote d'Ivoire
A/Cote D'Ivoire/1998/2015	EPI_ISL_215633	Africa	Cote d'Ivoire
A/Cote D'Ivoire/2045/2015	EPI_ISL_213979	Africa	Cote d'Ivoire
A/Cote D'Ivoire/2064/2015	EPI_ISL_215634	Africa	Cote d'Ivoire
A/Cote D'Ivoire/2109/2015	EPI_ISL_215635	Africa	Cote d'Ivoire
A/Cote D'Ivoire/2110/2015	EPI_ISL_215636	Africa	Cote d'Ivoire
A/Ethiopia/1140/2014	EPI_ISL_172733	Africa	Ethiopia
A/Ethiopia/1141/2014	EPI_ISL_171352	Africa	Ethiopia
A/Ethiopia/1146/2014	EPI_ISL_172532	Africa	Ethiopia
A/Ethiopia/1147/2014	EPI_ISL_172592	Africa	Ethiopia
A/Ethiopia/1153/2014	EPI_ISL_171380	Africa	Ethiopia
A/Ethiopia/1159/2014	EPI_ISL_172808	Africa	Ethiopia
A/Ethiopia/155/2014	EPI_ISL_172531	Africa	Ethiopia
A/Ethiopia/159/2014	EPI_ISL_172779	Africa	Ethiopia
A/Ethiopia/1797/2016	EPI_ISL_215779	Africa	Ethiopia
A/Ethiopia/1978/2016	EPI_ISL_230375	Africa	Ethiopia
A/Ethiopia/546/2014	EPI_ISL_171378	Africa	Ethiopia
A/Kenya/114/2016	EPI_ISL_249955	Africa	Kenya
A/Kenya/118/2013	EPI_ISL_149681	Africa	Kenya
A/Kenya/122/2014	EPI_ISL_171394	Africa	Kenya
A/Kenya/123/2014	EPI_ISL_171381	Africa	Kenya
A/Kenya/124/2014	EPI_ISL_171375	Africa	Kenya
A/Kenya/125/2014	EPI_ISL_171376	Africa	Kenya
A/Kenya/126/2014	EPI_ISL_171359	Africa	Kenya
A/Kenya/127/2014	EPI_ISL_171399	Africa	Kenya
A/Kenya/128/2014	EPI_ISL_171377	Africa	Kenya
A/Kenya/6063/2010	EPI_ISL_84053	Africa	Kenya
A/Mali/011 MOP/2015	EPI_ISL_211908	Africa	Mali
A/Mali/013 MOP/2015	EPI_ISL_211909	Africa	Mali

A/Mali/015 MOP/2015	EPI_ISL_211910	Africa	Mali
A/Mali/016 MOP/2015	EPI_ISL_211911	Africa	Mali
A/Mali/019 HGT/2015	EPI_ISL_211687	Africa	Mali
A/Mali/021 SIK/2015	EPI_ISL_206181	Africa	Mali
A/Mali/022 HGT/2015	EPI_ISL_212999	Africa	Mali
A/Mali/061 CS/2015	EPI_ISL_211690	Africa	Mali
A/Mali/067 CS/2015	EPI_ISL_211691	Africa	Mali
A/Mali/094 CH/2015	EPI_ISL_213000	Africa	Mali
A/Mali/101 CH/2015	EPI_ISL_224270	Africa	Mali
A/Mali/102 CH/2015	EPI_ISL_211688	Africa	Mali
A/Mali/102 CS/2015	EPI_ISL_206180	Africa	Mali
A/Mali/105 CH/2015	EPI_ISL_211681	Africa	Mali
A/Mali/106 CS/2015	EPI_ISL_206190	Africa	Mali
A/Mali/107 CI/2015	EPI_ISL_206168	Africa	Mali
A/Mali/107 CS/2015	EPI_ISL_206191	Africa	Mali
A/Mali/108 CI/2015	EPI_ISL_213001	Africa	Mali
A/Mali/108 CS/2015	EPI_ISL_206192	Africa	Mali
A/Mali/109 CH/2015	EPI_ISL_211693	Africa	Mali
A/Mali/109 CS/2015	EPI_ISL_206193	Africa	Mali
A/Mali/110 CH/2015	EPI_ISL_211685	Africa	Mali
A/Mali/112 CH/2015	EPI_ISL_213002	Africa	Mali
A/Mali/115 CI/2015	EPI_ISL_213003	Africa	Mali
A/Mali/117 CH/2015	EPI_ISL_211912	Africa	Mali
A/Mali/117 CI/2015	EPI_ISL_206170	Africa	Mali
A/Mali/117 CS/2015	EPI_ISL_206203	Africa	Mali
A/Mali/119 CS/2015	EPI_ISL_206208	Africa	Mali
A/Mali/120 CS/2015	EPI_ISL_207457	Africa	Mali
A/Mali/122 CI/2015	EPI_ISL_212366	Africa	Mali
A/Mali/125 CI/2015	EPI_ISL_213004	Africa	Mali
A/Mali/128 CI/2015	EPI_ISL_206172	Africa	Mali
A/Mali/13 HOP/2015	EPI_ISL_206198	Africa	Mali
A/Mali/130 CI/2015	EPI_ISL_211686	Africa	Mali
A/Mali/136 CI/2015	EPI_ISL_211694	Africa	Mali
A/Mali/141 CI/2015	EPI_ISL_211684	Africa	Mali
A/Mali/153 CI/2015	EPI_ISL_213005	Africa	Mali
A/Mali/174 CI/2015	EPI_ISL_211913	Africa	Mali
A/Mali/179 CH/2015	EPI_ISL_206174	Africa	Mali
A/Mali/182 CH/2015	EPI_ISL_206177	Africa	Mali
A/Mali/186 CH/2015	EPI_ISL_206178	Africa	Mali

A/Mali/187 CIV/2015	EPI_ISL_206179	Africa	Mali
A/Mali/193 CI/2015	EPI_ISL_206176	Africa	Mali
A/Mali/198 CH/2015	EPI_ISL_206197	Africa	Mali
A/Mali/202 CH/2015	EPI_ISL_207434	Africa	Mali
A/Mali/205 CI/2015	EPI_ISL_206183	Africa	Mali
A/Mali/206 CI/2015	EPI_ISL_206184	Africa	Mali
A/Mali/208 CI/2015	EPI_ISL_206185	Africa	Mali
A/Mali/209 CH/2015	EPI_ISL_206206	Africa	Mali
A/Mali/210 CI/2015	EPI_ISL_206186	Africa	Mali
A/Mali/214 CI/2015	EPI_ISL_206189	Africa	Mali
A/Mali/215 CH/2015	EPI_ISL_206211	Africa	Mali
A/Mali/215 CI/2015	EPI_ISL_206194	Africa	Mali
A/Mali/217 CI/2015	EPI_ISL_206195	Africa	Mali
A/Mali/218 CI/2015	EPI_ISL_206196	Africa	Mali
A/Mali/219 CH/2015	EPI_ISL_206216	Africa	Mali
A/Mali/22 SIK/2015	EPI_ISL_206182	Africa	Mali
A/Mali/229 CI/2015	EPI_ISL_207422	Africa	Mali
A/Mali/230 CI/2015	EPI_ISL_206200	Africa	Mali
A/Mali/231 CI/2015	EPI_ISL_206201	Africa	Mali
A/Mali/234 CI/2015	EPI_ISL_207395	Africa	Mali
A/Mali/236 CI/2015	EPI_ISL_206204	Africa	Mali
A/Mali/237 CI/2015	EPI_ISL_207455	Africa	Mali
A/Mali/238 CI/2015	EPI_ISL_207394	Africa	Mali
A/Mali/241 CI/2015	EPI_ISL_206207	Africa	Mali
A/Mali/244 CI/2015	EPI_ISL_206210	Africa	Mali
A/Mali/247 CI/2015	EPI_ISL_206214	Africa	Mali
A/Mali/29 MOP/2015	EPI_ISL_206173	Africa	Mali
A/Mali/30 HOP/2015	EPI_ISL_206213	Africa	Mali
A/Mali/30 SIK/2015	EPI_ISL_206199	Africa	Mali
A/Mali/45 CS/2015	EPI_ISL_206167	Africa	Mali
A/Mali/49 CS/2015	EPI_ISL_206169	Africa	Mali
A/Mali/56 CS/2015	EPI_ISL_206171	Africa	Mali
A/Mali/61 CH/2015	EPI_ISL_206166	Africa	Mali
A/Mali/81 CH/2015	EPI_ISL_225102	Africa	Mali
A/Mali/90 CS/2015	EPI_ISL_206175	Africa	Mali
A/Mayotte/2093/2016	EPI_ISL_331761	Africa	Mayotte
A/Moramanga/1942/2016	EPI_ISL_230306	Africa	Madagascar
A/Mozambique/207/2016	EPI_ISL_237366	Africa	Mozambique
A/Mozambique/415/2016	EPI_ISL_237367	Africa	Mozambique

A/MUWRP-Uganda/359/2012	EPI_ISL_381593	Africa	Uganda
A/MUWRP-Uganda/360/2012	EPI_ISL_381592	Africa	Uganda
A/MUWRP-Uganda/361/2012	EPI_ISL_381590	Africa	Uganda
A/MUWRP-Uganda/362/2012	EPI_ISL_381586	Africa	Uganda
A/MUWRP-Uganda/566/2015	EPI_ISL_381588	Africa	Uganda
A/MUWRP-Uganda/579/2016	EPI_ISL_381584	Africa	Uganda
A/MUWRP-Uganda/580/2016	EPI_ISL_381598	Africa	Uganda
A/Nigeria/120/2014	EPI_ISL_192158	Africa	Nigeria
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A/Nagasaki/14N024/2015	EPI_ISL_176857	Asia	Japan
A/Nagasaki/14N039/2015	EPI_ISL_176858	Asia	Japan
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A/Niigata/14F197/2015	EPI_ISL_176853	Asia	Japan
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A/Nonthaburi/333/2015	EPI_ISL_197257	Asia	Thailand
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A/Shanghai-Luwan/188/2011	EPI_ISL_94610	Asia	China
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A/Bethesda/NIH12/2011	EPI_ISL_179533	North America	United States
A/Bethesda/P0053/2015	EPI_ISL_253757	North America	United States
A/Boston/DOA09/2011	EPI_ISL_108090	North America	United States
A/Boston/DOA2-095/2012	EPI_ISL_147944	North America	United States
A/Boston/DOA2-098/2012	EPI_ISL_147947	North America	United States
A/Boston/DOA2-123/2012	EPI_ISL_147971	North America	United States
A/Boston/DOA2-127/2012	EPI_ISL_147975	North America	United States
A/Boston/DOA2-130/2012	EPI_ISL_147978	North America	United States
A/Boston/DOA2-136/2012	EPI_ISL_147984	North America	United States
A/Boston/DOA2-143/2012	EPI_ISL_147989	North America	United States
A/Boston/DOA2-145/2013	EPI_ISL_147991	North America	United States
A/Boston/DOA2-149/2013	EPI_ISL_147995	North America	United States
A/Boston/DOA2-151/2013	EPI_ISL_147997	North America	United States
A/Boston/DOA2-153/2013	EPI_ISL_147998	North America	United States
A/Boston/DOA2-159/2013	EPI_ISL_148004	North America	United States
A/Boston/DOA2-162/2012	EPI_ISL_148006	North America	United States
A/Boston/DOA2-166/2013	EPI_ISL_148008	North America	United States
A/Boston/DOA2-172/2013	EPI_ISL_148013	North America	United States
A/Boston/DOA2-182/2013	EPI_ISL_148023	North America	United States
A/Boston/DOA2-183/2013	EPI_ISL_148024	North America	United States
A/Boston/DOA2-184/2013	EPI_ISL_148025	North America	United States
A/Boston/DOA2-213/2013	EPI_ISL_148044	North America	United States
A/Boston/DOA2-217/2013	EPI_ISL_148047	North America	United States
A/Boston/DOA2-219/2012	EPI_ISL_148049	North America	United States
A/Boston/DOA2-225/2013	EPI_ISL_148055	North America	United States
A/Boston/DOA2-226/2013	EPI_ISL_148056	North America	United States

A/Boston/DOA2-230/2013	EPI_ISL_148060	North America	United States
A/Boston/DOA2-233/2013	EPI_ISL_148062	North America	United States
A/Boston/DOA2-236/2013	EPI_ISL_148064	North America	United States
A/Boston/DOA2-241/2013	EPI_ISL_148068	North America	United States
A/Boston/DOA2-246/2013	EPI_ISL_148073	North America	United States
A/Boston/DOA27/2011	EPI_ISL_128109	North America	United States
A/Boston/DOA38/2011	EPI_ISL_135252	North America	United States
A/Boston/DOA47/2011	EPI_ISL_135258	North America	United States
A/Boston/DOA48/2011	EPI_ISL_108176	North America	United States
A/Boston/DOA50/2011	EPI_ISL_135260	North America	United States
A/Boston/DOA60/2011	EPI_ISL_135263	North America	United States
A/Boston/DOA61/2011	EPI_ISL_108181	North America	United States
A/Boston/DOA82/2011	EPI_ISL_108238	North America	United States
A/Boston/YGA_00008/2012	EPI_ISL_160259	North America	United States
A/British Columbia/RV2358/2015	EPI_ISL_202413	North America	Canada
A/California/106/2015	EPI_ISL_205665	North America	United States
A/California/11/2016	EPI_ISL_212964	North America	United States
A/California/118/2015	EPI_ISL_207016	North America	United States
A/California/121/2015	EPI_ISL_208601	North America	United States
A/California/133/2015	EPI_ISL_214525	North America	United States
A/California/15/2014	EPI_ISL_167915	North America	United States
A/California/154/2016	EPI_ISL_239166	North America	United States
A/California/16/2015	EPI_ISL_251360	North America	United States
A/California/17/2014	EPI_ISL_167917	North America	United States
A/California/198/2016	EPI_ISL_242752	North America	United States
A/California/209/2016	EPI_ISL_244689	North America	United States
A/California/24/2016	EPI_ISL_212969	North America	United States
A/California/74/2016	EPI_ISL_222008	North America	United States
A/California/93/2015	EPI_ISL_202935	North America	United States
A/California/95/2015	EPI_ISL_202937	North America	United States
A/California/BRD11499N/2012	EPI_ISL_235219	North America	United States
A/California/NHRC0003/2011	EPI_ISL_91033	North America	United States
A/Colorado/38/2012	EPI_ISL_235249	North America	United States
A/Columbia/P0033/2014	EPI_ISL_253820	North America	United States
A/Columbia/P0090/2015	EPI_ISL_253810	North America	United States
A/Connecticut/20/2016	EPI_ISL_225098	North America	United States
A/Connecticut/21/2014	EPI_ISL_249815	North America	United States
A/Connecticut/44/2016	EPI_ISL_248009	North America	United States
A/Connecticut/Flu060/2012	EPI_ISL_202144	North America	United States

A/Connecticut/Flu099/2013	EPI_ISL_202149	North America	United States
A/Costa Rica/1172/2016	EPI_ISL_249023	North America	Costa Rica
A/Costa Rica/2536/2016	EPI_ISL_238648	North America	Costa Rica
A/Costa Rica/4582/2015	EPI_ISL_212056	North America	Costa Rica
A/Costa Rica/7141/2015	EPI_ISL_212057	North America	Costa Rica
A/Costa Rica/9930/2015	EPI_ISL_212159	North America	Costa Rica
A/Delaware/12/2015	EPI_ISL_176558	North America	United States
A/Delaware/13/2015	EPI_ISL_251328	North America	United States
A/Delaware/15/2012	EPI_ISL_134451	North America	United States
A/Delaware/43/2015	EPI_ISL_206160	North America	United States
A/District of Columbia/WRAIR0300/2010	EPI_ISL_93639	North America	United States
A/Dominica/672/2015	EPI_ISL_194947	North America	Dominica
A/Dominica/8432/2016	EPI_ISL_240327	North America	Dominica
A/Dominican Republic/9441/2015	EPI_ISL_215255	North America	Dominican Republic
A/Florida/06/2016	EPI_ISL_219168	North America	United States
A/Florida/09/2016	EPI_ISL_213982	North America	United States
A/Florida/11/2015	EPI_ISL_251228	North America	United States
A/Florida/15/2016	EPI_ISL_213984	North America	United States
A/Florida/18/2015	EPI_ISL_251284	North America	United States
A/Florida/20/2015	EPI_ISL_236777	North America	United States
A/Florida/39/2014	EPI_ISL_167414	North America	United States
A/Florida/65/2014	EPI_ISL_250965	North America	United States
A/Florida/68/2016	EPI_ISL_230348	North America	United States
A/Florida/70/2015	EPI_ISL_205246	North America	United States
A/Florida/76/2014	EPI_ISL_251004	North America	United States
A/Florida/78/2016	EPI_ISL_237330	North America	United States
A/Florida/88/2016	EPI_ISL_239178	North America	United States
A/Florida/89/2015	EPI_ISL_207026	North America	United States
A/Florida/91/2016	EPI_ISL_239691	North America	United States
A/Florida/92/2016	EPI_ISL_239692	North America	United States
A/Gainesville/09/2016	EPI_ISL_258586	North America	United States
A/Georgia/24/2014	EPI_ISL_250955	North America	United States
A/Georgia/52/2016	EPI_ISL_224017	North America	United States
A/Georgia/54/2016	EPI_ISL_225043	North America	United States
A/Guadeloupe/7129/2016	EPI_ISL_233431	North America	Guadeloupe
A/Guatemala/15/2015	EPI_ISL_197555	North America	Guatemala
A/Guatemala/4084/2015	EPI_ISL_212985	North America	Guatemala
A/Guatemala/4392/2016	EPI_ISL_233438	North America	Guatemala
A/Guatemala/5211/2014	EPI_ISL_172535	North America	Guatemala

A/Hawaii/04/2016	EPI_ISL_219160	North America	United States
A/Hawaii/103/2016	EPI_ISL_242760	North America	United States
A/Hawaii/16/2016	EPI_ISL_219211	North America	United States
A/Hawaii/22/2012	EPI_ISL_129859	North America	United States
A/Hawaii/64/2015	EPI_ISL_203564	North America	United States
A/Hawaii/67/2015	EPI_ISL_202110	North America	United States
A/Hawaii/74/2015	EPI_ISL_202921	North America	United States
A/Hawaii/75/2016	EPI_ISL_237314	North America	United States
A/Hawaii/76/2016	EPI_ISL_237313	North America	United States
A/Hawaii/80/2015	EPI_ISL_212161	North America	United States
A/Houston/JMM_105/2013	EPI_ISL_189231	North America	United States
A/Houston/JMM_108/2013	EPI_ISL_189293	North America	United States
A/Houston/JMM_115/2013	EPI_ISL_189270	North America	United States
A/Houston/JMM_119/2013	EPI_ISL_189274	North America	United States
A/Houston/JMM_125/2013	EPI_ISL_189280	North America	United States
A/Houston/JMM_132/2013	EPI_ISL_189287	North America	United States
A/Houston/JMM_147/2013	EPI_ISL_189307	North America	United States
A/Houston/JMM_151/2013	EPI_ISL_189643	North America	United States
A/Houston/JMM_153/2013	EPI_ISL_189617	North America	United States
A/Houston/JMM_160/2013	EPI_ISL_189624	North America	United States
A/Houston/JMM_164/2013	EPI_ISL_189628	North America	United States
A/Houston/JMM_169/2013	EPI_ISL_189632	North America	United States
A/Houston/JMM_170/2013	EPI_ISL_189633	North America	United States
A/Houston/JMM_174/2013	EPI_ISL_189636	North America	United States
A/Houston/JMM_176/2013	EPI_ISL_189638	North America	United States
A/Houston/JMM_180/2013	EPI_ISL_189642	North America	United States
A/Houston/JMM_69/2012	EPI_ISL_189198	North America	United States
A/Houston/JMM_75/2012	EPI_ISL_189203	North America	United States
A/Houston/JMM_84/2012	EPI_ISL_189212	North America	United States
A/Idaho/01/2015	EPI_ISL_174142	North America	United States
A/Idaho/14/2016	EPI_ISL_219270	North America	United States
A/Illinois/03/2013	EPI_ISL_145067	North America	United States
A/Illinois/11/2012	EPI_ISL_129021	North America	United States
A/Illinois/19/2012	EPI_ISL_235313	North America	United States
A/Illinois/45/2016	EPI_ISL_237344	North America	United States
A/Illinois/50/2016	EPI_ISL_247995	North America	United States
A/Illinois/58/2016	EPI_ISL_253566	North America	United States
A/Illinois/NHRC0002/2011	EPI_ISL_90553	North America	United States
A/Indiana/08/2011	EPI_ISL_99419	North America	United States

A/Indiana/125/2012	EPI_ISL_129421	North America	United States
A/Indiana/135/2012	EPI_ISL_129425	North America	United States
A/Indiana/15/2012	EPI_ISL_126254	North America	United States
A/Indiana/152/2012	EPI_ISL_129170	North America	United States
A/Indiana/29/2015	EPI_ISL_206121	North America	United States
A/Indiana/30/2016	EPI_ISL_219260	North America	United States
A/Indiana/57/2012	EPI_ISL_129417	North America	United States
A/Indiana/65/2012	EPI_ISL_128352	North America	United States
A/Indiana/77/2012	EPI_ISL_129410	North America	United States
A/Iowa/10/2016	EPI_ISL_220365	North America	United States
A/Iowa/14/2012	EPI_ISL_131825	North America	United States
A/Iowa/19/2010	EPI_ISL_93788	North America	United States
A/Iowa/23/2016	EPI_ISL_234047	North America	United States
A/Iowa/33/2016	EPI_ISL_239186	North America	United States
A/Iowa/37/2015	EPI_ISL_197546	North America	United States
A/Iowa/50/2015	EPI_ISL_202088	North America	United States
A/Iowa/54/2015	EPI_ISL_203414	North America	United States
A/Kansas/08/2015	EPI_ISL_251290	North America	United States
A/Kentucky/01/2015	EPI_ISL_251260	North America	United States
A/Kentucky/21/2014	EPI_ISL_251121	North America	United States
A/Louisiana/08/2015	EPI_ISL_211703	North America	United States
A/Louisiana/12/2016	EPI_ISL_220372	North America	United States
A/Louisiana/13/2014	EPI_ISL_250219	North America	United States
A/Louisiana/13/2016	EPI_ISL_220373	North America	United States
A/Maine/04/2014	EPI_ISL_167411	North America	United States
A/Maine/06/2011	EPI_ISL_97361	North America	United States
A/Managua/1181.03/2010	EPI_ISL_78770	North America	Nicaragua
A/Managua/1856.03/2010	EPI_ISL_80848	North America	Nicaragua
A/Managua/2654.01/2010	EPI_ISL_89577	North America	Nicaragua
A/Managua/3209.01/2010	EPI_ISL_89669	North America	Nicaragua
A/Managua/3570.04/2010	EPI_ISL_80864	North America	Nicaragua
A/Managua/5444.02/2010	EPI_ISL_89587	North America	Nicaragua
A/Managua/8779.06/2016	EPI_ISL_238659	North America	Nicaragua
A/Managua/905.02/2010	EPI_ISL_80843	North America	Nicaragua
A/Maryland/01/2015	EPI_ISL_236786	North America	United States
A/Maryland/118_10D/2013	EPI_ISL_368546	North America	United States
A/Maryland/12/2015	EPI_ISL_251666	North America	United States
A/Maryland/131_10D/2013	EPI_ISL_368552	North America	United States
A/Maryland/136_8/2013	EPI_ISL_368554	North America	United States

A/Maryland/138_15D/2013	EPI_ISL_370292	North America	United States
A/Maryland/153_1/2013	EPI_ISL_368563	North America	United States
A/Maryland/153_5D/2013	EPI_ISL_368564	North America	United States
A/Maryland/165_2/2013	EPI_ISL_370302	North America	United States
A/Maryland/176_12/2013	EPI_ISL_368567	North America	United States
A/Maryland/18/2015	EPI_ISL_202425	North America	United States
A/Maryland/187_7/2013	EPI_ISL_368569	North America	United States
A/Maryland/242_5D/2013	EPI_ISL_370313	North America	United States
A/Maryland/25/2012	EPI_ISL_129176	North America	United States
A/Maryland/277_7A/2013	EPI_ISL_370315	North America	United States
A/Maryland/31_7/2012	EPI_ISL_368585	North America	United States
A/Maryland/48_5D/2013	EPI_ISL_368588	North America	United States
A/Maryland/54_1/2013	EPI_ISL_368591	North America	United States
A/Maryland/63_11D/2013	EPI_ISL_368596	North America	United States
A/Maryland/63_13/2013	EPI_ISL_368597	North America	United States
A/Maryland/63_16/2013	EPI_ISL_370324	North America	United States
A/Maryland/66_9/2013	EPI_ISL_370327	North America	United States
A/Maryland/68_8/2013	EPI_ISL_368602	North America	United States
A/Maryland/79_1/2013	EPI_ISL_368604	North America	United States
A/Maryland/84_1/2013	EPI_ISL_368609	North America	United States
A/Maryland/84_7/2013	EPI_ISL_368610	North America	United States
A/Maryland/88_1/2013	EPI_ISL_368611	North America	United States
A/Maryland/92_5D/2013	EPI_ISL_368616	North America	United States
A/Maryland/97_12/2013	EPI_ISL_368618	North America	United States
A/Maryland/97_9/2013	EPI_ISL_355174	North America	United States
A/Masaya/INI00222/2011	EPI_ISL_235304	North America	Nicaragua
A/Massachusetts/05/2015	EPI_ISL_176537	North America	United States
A/Massachusetts/09/2015	EPI_ISL_251289	North America	United States
A/Massachusetts/15/2015	EPI_ISL_181072	North America	United States
A/Mexico City/WRAIR1752T/2010	EPI_ISL_93658	North America	Mexico
A/Mexico City/WRAIR3568N/2010	EPI_ISL_93669	North America	Mexico
A/Mexico City/WRAIR3569N/2010	EPI_ISL_95501	North America	Mexico
A/Mexico City/WRAIR4139N/2010	EPI_ISL_93681	North America	Mexico
A/Mexico/1402/2015	EPI_ISL_197532	North America	Mexico
A/Mexico/2377/2015	EPI_ISL_219153	North America	Mexico
A/Mexico/836/2014	EPI_ISL_172786	North America	Mexico
A/Michigan/09/2014	EPI_ISL_249784	North America	United States
A/Michigan/105/2016	EPI_ISL_237332	North America	United States
A/Michigan/16/2012	EPI_ISL_129620	North America	United States

A/Michigan/24/2016	EPI_ISL_215260	North America	United States
A/Michigan/29/2016	EPI_ISL_214538	North America	United States
A/Michigan/58/2015	EPI_ISL_202903	North America	United States
A/Minnesota/22/2014	EPI_ISL_249770	North America	United States
A/Minnesota/25/2015	EPI_ISL_251750	North America	United States
A/Minnesota/43/2015	EPI_ISL_201306	North America	United States
A/Minnesota/72/2016	EPI_ISL_237318	North America	United States
A/Minnesota/83/2016	EPI_ISL_258291	North America	United States
A/Minnesota/85/2016	EPI_ISL_241631	North America	United States
A/Mississippi/12/2014	EPI_ISL_250362	North America	United States
A/Missouri/11/2015	EPI_ISL_237206	North America	United States
A/Montana/11/2014	EPI_ISL_250289	North America	United States
A/Montana/19/2015	EPI_ISL_200750	North America	United States
A/Montana/21/2015	EPI_ISL_200752	North America	United States
A/Montana/24/2015	EPI_ISL_203418	North America	United States
A/Montana/27/2014	EPI_ISL_251033	North America	United States
A/Montana/32/2015	EPI_ISL_201283	North America	United States
A/Montana/62/2016	EPI_ISL_240184	North America	United States
A/Nebraska/10/2016	EPI_ISL_214542	North America	United States
A/Nebraska/15/2014	EPI_ISL_251007	North America	United States
A/Nebraska/20/2012	EPI_ISL_235314	North America	United States
A/Nevada/18/2014	EPI_ISL_250343	North America	United States
A/Nevada/21/2016	EPI_ISL_219273	North America	United States
A/Nevada/22/2016	EPI_ISL_219238	North America	United States
A/Nevada/25usafsam/2012	EPI_ISL_235319	North America	United States
A/New Hampshire/32/2014	EPI_ISL_250956	North America	United States
A/New Jersey/28/2016	EPI_ISL_244791	North America	United States
A/New Jersey/52/2015	EPI_ISL_201254	North America	United States
A/New Mexico/06/2016	EPI_ISL_215641	North America	United States
A/New Mexico/54/2016	EPI_ISL_240847	North America	United States
A/New York/03/2016	EPI_ISL_211916	North America	United States
A/New York/100/2016	EPI_ISL_238679	North America	United States
A/New York/111/2016	EPI_ISL_249062	North America	United States
A/New York/112/2016	EPI_ISL_241558	North America	United States
A/New York/39/2012	EPI_ISL_164405	North America	United States
A/New York/76/2015	EPI_ISL_211918	North America	United States
A/New York/96/2016	EPI_ISL_235536	North America	United States
A/New York/A-WC-LVD-16-001/2016	EPI_ISL_293361	North America	United States
A/New York/WC-LVD-10-008/2010	EPI_ISL_369514	North America	United States

A/New York/WC-LVD-10-009/2010	EPI_ISL_369515	North America	United States
A/New York/WC-LVD-11-006/2011	EPI_ISL_369523	North America	United States
A/New York/WC-LVD-11-007/2011	EPI_ISL_369524	North America	United States
A/New York/WC-LVD-11-010/2011	EPI_ISL_369527	North America	United States
A/New York/WC-LVD-11-011/2011	EPI_ISL_369528	North America	United States
A/New York/WC-LVD-11-015/2011	EPI_ISL_369532	North America	United States
A/New York/WC-LVD-12-002/2012	EPI_ISL_369537	North America	United States
A/New York/WC-LVD-12-005/2012	EPI_ISL_369540	North America	United States
A/New York/WC-LVD-12-015/2012	EPI_ISL_369549	North America	United States
A/New York/WC-LVD-12-018/2012	EPI_ISL_369552	North America	United States
A/New York/WC-LVD-12-020/2012	EPI_ISL_369554	North America	United States
A/New York/WC-LVD-12-053/2012	EPI_ISL_369560	North America	United States
A/New York/WC-LVD-12-054/2012	EPI_ISL_369561	North America	United States
A/New York/WC-LVD-12-060/2012	EPI_ISL_369566	North America	United States
A/New York/WC-LVD-12-063/2012	EPI_ISL_369569	North America	United States
A/New York/WC-LVD-12-065/2012	EPI_ISL_369571	North America	United States
A/New York/WC-LVD-12-068/2012	EPI_ISL_369574	North America	United States
A/New York/WC-LVD-12-075/2012	EPI_ISL_369581	North America	United States
A/New York/WC-LVD-12-078/2012	EPI_ISL_369584	North America	United States
A/New York/WC-LVD-12-079/2012	EPI_ISL_369585	North America	United States
A/New York/WC-LVD-12-080/2012	EPI_ISL_369586	North America	United States
A/New York/WC-LVD-12-090/2012	EPI_ISL_369594	North America	United States
A/New York/WC-LVD-13-031/2013	EPI_ISL_369595	North America	United States
A/New York/WC-LVD-13-044/2013	EPI_ISL_369605	North America	United States
A/New York/WC-LVD-14-102/2014	EPI_ISL_235692	North America	United States
A/New York/WC-LVD-15-012/2015	EPI_ISL_235644	North America	United States
A/New York/WC-LVD-15-031/2015	EPI_ISL_235667	North America	United States
A/New York/WC-LVD-15-039/2015	EPI_ISL_235674	North America	United States
A/New York/WC-LVD-15-044/2015	EPI_ISL_235679	North America	United States
A/Nicaragua/30014_01_TR2/2012	EPI_ISL_174231	North America	Nicaragua
A/Nicaragua/30143_01_tr3/2013	EPI_ISL_174235	North America	Nicaragua
A/Nicaragua/4877_07/2014	EPI_ISL_279367	North America	Nicaragua
A/Nicaragua/5465_01_TR3/2013	EPI_ISL_174243	North America	Nicaragua
A/Nicaragua/5627_04/2014	EPI_ISL_279366	North America	Nicaragua
A/Nicaragua/5867_01/2010	EPI_ISL_279387	North America	Nicaragua
A/Nicaragua/5929_02/2010	EPI_ISL_279392	North America	Nicaragua
A/Nicaragua/6006_02/2010	EPI_ISL_279394	North America	Nicaragua
A/Nicaragua/6200_06/2014	EPI_ISL_279372	North America	Nicaragua
A/Nicaragua/6530_19/2014	EPI_ISL_279371	North America	Nicaragua

A/Nicaragua/6597_07/2014	EPI_ISL_279376	North America	Nicaragua
A/Nicaragua/6826_06/2014	EPI_ISL_279355	North America	Nicaragua
A/Nicaragua/6831.07/2016	EPI_ISL_257874	North America	Nicaragua
A/Nicaragua/930_01_TR1/2012	EPI_ISL_174232	North America	Nicaragua
A/Nicaragua/AGA2-101/2012	EPI_ISL_189139	North America	Nicaragua
A/Nicaragua/AGA2-103/2012	EPI_ISL_189141	North America	Nicaragua
A/Nicaragua/AGA2-14/2012	EPI_ISL_188992	North America	Nicaragua
A/Nicaragua/AGA2-17/2012	EPI_ISL_188993	North America	Nicaragua
A/Nicaragua/AGA2-18/2012	EPI_ISL_188994	North America	Nicaragua
A/Nicaragua/AGA2-21/2012	EPI_ISL_188997	North America	Nicaragua
A/Nicaragua/AGA2-67/2011	EPI_ISL_189086	North America	Nicaragua
A/Nicaragua/AGA2-72/2012	EPI_ISL_189090	North America	Nicaragua
A/Nicaragua/AGA2-84/2012	EPI_ISL_189099	North America	Nicaragua
A/Nicaragua/AGA2-93/2012	EPI_ISL_189107	North America	Nicaragua
A/North Carolina/05/2015	EPI_ISL_251159	North America	United States
A/North Carolina/16/2015	EPI_ISL_251580	North America	United States
A/North Carolina/41/2016	EPI_ISL_225060	North America	United States
A/North Dakota/05/2015	EPI_ISL_251270	North America	United States
A/Northwest Territories/RV2421/2015	EPI_ISL_207440	North America	Canada
A/Ohio/04/2015	EPI_ISL_251287	North America	United States
A/Ohio/19/2012	EPI_ISL_129755	North America	United States
A/Ohio/20/2016	EPI_ISL_224046	North America	United States
A/Ohio/27/2016	EPI_ISL_232044	North America	United States
A/Ohio/47/2012	EPI_ISL_129649	North America	United States
A/Ohio/63/2012	EPI_ISL_129429	North America	United States
A/Ohio/77/2012	EPI_ISL_129411	North America	United States
A/Ohio/86/2012	EPI_ISL_129653	North America	United States
A/Ohio/88/2012	EPI_ISL_129758	North America	United States
A/Oklahoma/06/2015	EPI_ISL_251339	North America	United States
A/Oklahoma/18/2016	EPI_ISL_240224	North America	United States
A/Oklahoma/31/2012	EPI_ISL_235245	North America	United States
A/Ontario/RV3236/2016	EPI_ISL_239893	North America	Canada
A/Ontario/RV3606/2014	EPI_ISL_171398	North America	Canada
A/Oregon/05/2015	EPI_ISL_251658	North America	United States
A/Oregon/05/2016	EPI_ISL_215797	North America	United States
A/Oregon/21/2016	EPI_ISL_239209	North America	United States
A/Oregon/24/2015	EPI_ISL_201292	North America	United States
A/Panama/307149/2010	EPI_ISL_79320	North America	Panama
A/Pennsylvania/09/2011	EPI_ISL_96012	North America	United States

A/Pennsylvania/10/2015	EPI_ISL_251166	North America	United States
A/Pennsylvania/113/2016	EPI_ISL_249088	North America	United States
A/Pennsylvania/137/2016	EPI_ISL_289309	North America	United States
A/Pennsylvania/17/2012	EPI_ISL_129189	North America	United States
A/Pennsylvania/20/2016	EPI_ISL_219241	North America	United States
A/Pennsylvania/28/2014	EPI_ISL_286142	North America	United States
A/Puerto Rico/35/2015	EPI_ISL_206222	North America	Puerto Rico
A/Puerto Rico/37/2015	EPI_ISL_206224	North America	Puerto Rico
A/Puerto Rico/44/2015	EPI_ISL_206229	North America	Puerto Rico
A/Quebec/RV3242/2016	EPI_ISL_244890	North America	Canada
A/Rhode Island/15/2015	EPI_ISL_251702	North America	United States
A/Rhode Island/29/2016	EPI_ISL_235112	North America	United States
A/South Carolina/07/2015	EPI_ISL_251318	North America	United States
A/South Dakota/01/2015	EPI_ISL_251163	North America	United States
A/South Dakota/27/2016	EPI_ISL_239211	North America	United States
A/South Dakota/40/2015	EPI_ISL_206132	North America	United States
A/Tennessee/02/2016	EPI_ISL_214551	North America	United States
A/Tennessee/09/2015	EPI_ISL_251407	North America	United States
A/Tennessee/15/2014	EPI_ISL_251030	North America	United States
A/Tennessee/18/2015	EPI_ISL_200727	North America	United States
A/Tennessee/41/2016	EPI_ISL_253622	North America	United States
A/Tennessee/F2018A/2011	EPI_ISL_158625	North America	United States
A/Tennessee/F2019A/2011	EPI_ISL_158627	North America	United States
A/Tennessee/F2031A/2011	EPI_ISL_158632	North America	United States
A/Tennessee/F2048/2011	EPI_ISL_158662	North America	United States
A/Tennessee/F2053/2011	EPI_ISL_158664	North America	United States
A/Tennessee/F2078A/2011	EPI_ISL_158672	North America	United States
A/Tennessee/F2079B/2011	EPI_ISL_158675	North America	United States
A/Texas/158/2016	EPI_ISL_232102	North America	United States
A/Texas/170/2016	EPI_ISL_230319	North America	United States
A/Texas/201/2016	EPI_ISL_241573	North America	United States
A/Texas/28/2015	EPI_ISL_237203	North America	United States
A/Texas/30/2016	EPI_ISL_214554	North America	United States
A/Texas/42/2016	EPI_ISL_215645	North America	United States
A/Texas/83/2016	EPI_ISL_220296	North America	United States
A/Texas/84/2014	EPI_ISL_251154	North America	United States
A/Texas/JMM_15/2012	EPI_ISL_136451	North America	United States
A/Texas/JMM_16/2012	EPI_ISL_136452	North America	United States
A/Texas/JMM_18/2012	EPI_ISL_136454	North America	United States

A/Texas/JMM_19/2012	EPI_ISL_136455	North America	United States
A/Texas/JMM_21/2012	EPI_ISL_136457	North America	United States
A/Texas/JMM_26/2012	EPI_ISL_136481	North America	United States
A/Texas/JMM_3/2012	EPI_ISL_136441	North America	United States
A/Texas/JMM_32/2012	EPI_ISL_136486	North America	United States
A/Texas/JMM_33/2012	EPI_ISL_136487	North America	United States
A/Texas/JMM_35/2012	EPI_ISL_136489	North America	United States
A/Texas/JMM_37/2012	EPI_ISL_136491	North America	United States
A/Texas/JMM_45/2012	EPI_ISL_136498	North America	United States
A/Texas/JMM_51/2012	EPI_ISL_136504	North America	United States
A/Texas/JMM_59/2012	EPI_ISL_136511	North America	United States
A/Utah/12/2016	EPI_ISL_214013	North America	United States
A/Utah/33/2014	EPI_ISL_251027	North America	United States
A/Vermont/16/2016	EPI_ISL_223190	North America	United States
A/Vermont/32/2016	EPI_ISL_238715	North America	United States
A/Vermont/34/2016	EPI_ISL_247989	North America	United States
A/Virginia/03/2015	EPI_ISL_251190	North America	United States
A/Virginia/42/2014	EPI_ISL_250995	North America	United States
A/Virginia/63/2016	EPI_ISL_239731	North America	United States
A/Virginia/69/2016	EPI_ISL_253572	North America	United States
A/Washington/120/2016	EPI_ISL_286325	North America	United States
A/Washington/128/2016	EPI_ISL_286332	North America	United States
A/Washington/13/2015	EPI_ISL_251347	North America	United States
A/Washington/144/2016	EPI_ISL_286363	North America	United States
A/Washington/153/2016	EPI_ISL_286365	North America	United States
A/Washington/35/2015	EPI_ISL_251664	North America	United States
A/Washington/45/2015	EPI_ISL_202841	North America	United States
A/Washington/46/2014	EPI_ISL_251115	North America	United States
A/Washington/49/2015	EPI_ISL_202101	North America	United States
A/Washington/55/2016	EPI_ISL_222075	North America	United States
A/Washington/60/2015	EPI_ISL_206122	North America	United States
A/Washington/61/2015	EPI_ISL_205628	North America	United States
A/Washington/87/2016	EPI_ISL_248366	North America	United States
A/West Virginia/15/2016	EPI_ISL_248300	North America	United States
A/Wisconsin/23/2012	EPI_ISL_129022	North America	United States
A/Wisconsin/75/2014	EPI_ISL_251097	North America	United States
A/Wisconsin/77/2016	EPI_ISL_234055	North America	United States
A/Wisconsin/82/2015	EPI_ISL_205256	North America	United States
A/Wisconsin/86/2015	EPI_ISL_202431	North America	United States

A/Wisconsin/95/2016	EPI_ISL_248362	North America	United States
A/Acre/133946-IEC/2015	EPI_ISL_200698	South America	Brazil
A/Acre/134806-IEC/2015	EPI_ISL_201222	South America	Brazil
A/Acre/135094-IEC/2015	EPI_ISL_201223	South America	Brazil
A/Acre/135356-IEC/2015	EPI_ISL_201225	South America	Brazil
A/Alegrete/LACENRS-1624/2014	EPI_ISL_263261	South America	Brazil
A/Argentina/103/2015	EPI_ISL_205197	South America	Argentina
A/Argentina/104/2015	EPI_ISL_205199	South America	Argentina
A/Argentina/11071/2014	EPI_ISL_167908	South America	Argentina
A/Argentina/11093/2014	EPI_ISL_167909	South America	Argentina
A/Argentina/11126/2014	EPI_ISL_167910	South America	Argentina
A/Argentina/112/2015	EPI_ISL_200730	South America	Argentina
A/Argentina/113/2015	EPI_ISL_200731	South America	Argentina
A/Argentina/114/2015	EPI_ISL_200732	South America	Argentina
A/Argentina/11573/2015	EPI_ISL_200742	South America	Argentina
A/Argentina/11592/2015	EPI_ISL_205201	South America	Argentina
A/Argentina/11594/2015	EPI_ISL_205203	South America	Argentina
A/Argentina/11596/2015	EPI_ISL_205205	South America	Argentina
A/Argentina/116/2015	EPI_ISL_202387	South America	Argentina
A/Argentina/116/2016	EPI_ISL_230315	South America	Argentina
A/Argentina/11611/2015	EPI_ISL_205207	South America	Argentina
A/Argentina/11628/2015	EPI_ISL_205209	South America	Argentina
A/Argentina/11639/2015	EPI_ISL_205210	South America	Argentina
A/Argentina/11640/2015	EPI_ISL_205213	South America	Argentina
A/Argentina/11652/2015	EPI_ISL_205215	South America	Argentina
A/Argentina/11656/2015	EPI_ISL_205217	South America	Argentina
A/Argentina/11659/2015	EPI_ISL_205219	South America	Argentina
A/Argentina/120/2015	EPI_ISL_200734	South America	Argentina
A/Argentina/121/2015	EPI_ISL_200735	South America	Argentina
A/Argentina/132/2015	EPI_ISL_200736	South America	Argentina
A/Argentina/133/2015	EPI_ISL_200737	South America	Argentina
A/Argentina/135/2015	EPI_ISL_195879	South America	Argentina
A/Argentina/149/2015	EPI_ISL_202434	South America	Argentina
A/Argentina/156/2015	EPI_ISL_202435	South America	Argentina
A/Argentina/157/2015	EPI_ISL_202437	South America	Argentina
A/Argentina/158/2015	EPI_ISL_202438	South America	Argentina
A/Argentina/163/2015	EPI_ISL_202829	South America	Argentina
A/Argentina/166/2015	EPI_ISL_195878	South America	Argentina
A/Argentina/169/2015	EPI_ISL_202831	South America	Argentina

A/Argentina/181/2015	EPI_ISL_202833	South America	Argentina
A/Argentina/183/2015	EPI_ISL_195866	South America	Argentina
A/Argentina/196/2015	EPI_ISL_195873	South America	Argentina
A/Argentina/218/2015	EPI_ISL_195875	South America	Argentina
A/Argentina/229/2015	EPI_ISL_195857	South America	Argentina
A/Argentina/23/2015	EPI_ISL_205191	South America	Argentina
A/Argentina/234/2015	EPI_ISL_195877	South America	Argentina
A/Argentina/235/2015	EPI_ISL_195860	South America	Argentina
A/Argentina/236/2015	EPI_ISL_195861	South America	Argentina
A/Argentina/24/2015	EPI_ISL_205193	South America	Argentina
A/Argentina/25/2015	EPI_ISL_205195	South America	Argentina
A/Argentina/250/2015	EPI_ISL_195864	South America	Argentina
A/Argentina/254/2015	EPI_ISL_195863	South America	Argentina
A/Argentina/255/2015	EPI_ISL_195867	South America	Argentina
A/Argentina/261/2015	EPI_ISL_195871	South America	Argentina
A/Argentina/943/2016	EPI_ISL_230314	South America	Argentina
A/Bage/LACENRS-1200/2014	EPI_ISL_263274	South America	Brazil
A/Bage/LACENRS-2050/2013	EPI_ISL_263254	South America	Brazil
A/Bogota/WRAIR3457N/2010	EPI_ISL_93662	South America	Colombia
A/Bogota/WRAIR3457T/2010	EPI_ISL_93663	South America	Colombia
A/Bolivia/1770/2016	EPI_ISL_238657	South America	Bolivia
A/Bolivia/2315/2016	EPI_ISL_239165	South America	Bolivia
A/Bolivia/426/2015	EPI_ISL_205276	South America	Bolivia
A/Bolivia/499/2015	EPI_ISL_205277	South America	Bolivia
A/Bolivia/502/2015	EPI_ISL_205278	South America	Bolivia
A/Bolivia/667/2014	EPI_ISL_167911	South America	Bolivia
A/Bolivia/716/2014	EPI_ISL_167912	South America	Bolivia
A/Bolivia/751/2014	EPI_ISL_167913	South America	Bolivia
A/Bom Retiro do Sul/LACENRS-3406/2013	EPI_ISL_263123	South America	Brazil
A/Brazil/0168/2015	EPI_ISL_201246	South America	Brazil
A/Brazil/0293/2016	EPI_ISL_232999	South America	Brazil
A/Brazil/0507/2015	EPI_ISL_206124	South America	Brazil
A/Brazil/0515/2015	EPI_ISL_206125	South America	Brazil
A/Brazil/0523/2015	EPI_ISL_206123	South America	Brazil
A/Brazil/0636/2015	EPI_ISL_206126	South America	Brazil
A/Brazil/0640/2015	EPI_ISL_206127	South America	Brazil
A/Brazil/0769/2014	EPI_ISL_168112	South America	Brazil
A/Brazil/0809/2016	EPI_ISL_244823	South America	Brazil
A/Brazil/114/2015	EPI_ISL_197556	South America	Brazil

A/Brazil/1790/2015	EPI_ISL_201247	South America	Brazil
A/Brazil/1804/2015	EPI_ISL_200673	South America	Brazil
A/Brazil/187/2015	EPI_ISL_193330	South America	Brazil
A/Brazil/2002/2015	EPI_ISL_202400	South America	Brazil
A/Brazil/2035/2014	EPI_ISL_168119	South America	Brazil
A/Brazil/2047/2015	EPI_ISL_201249	South America	Brazil
A/Brazil/2081/2015	EPI_ISL_201248	South America	Brazil
A/Brazil/23262/2015	EPI_ISL_212137	South America	Brazil
A/Brazil/237/2015	EPI_ISL_194174	South America	Brazil
A/Brazil/2837/2015	EPI_ISL_197256	South America	Brazil
A/Brazil/367/2014	EPI_ISL_168121	South America	Brazil
A/Brazil/3972/2014	EPI_ISL_168104	South America	Brazil
A/Brazil/4146/2014	EPI_ISL_168128	South America	Brazil
A/Brazil/4388/2015	EPI_ISL_201245	South America	Brazil
A/Brazil/4390/2015	EPI_ISL_202397	South America	Brazil
A/Brazil/440/2015	EPI_ISL_200674	South America	Brazil
A/Brazil/4996/2015	EPI_ISL_200677	South America	Brazil
A/Brazil/56/2015	EPI_ISL_195885	South America	Brazil
A/Brazil/6069/2014	EPI_ISL_168123	South America	Brazil
A/Brazil/623/2014	EPI_ISL_168120	South America	Brazil
A/Brazil/6261/2015	EPI_ISL_200678	South America	Brazil
A/Brazil/6359/2016	EPI_ISL_242690	South America	Brazil
A/Brazil/70/2015	EPI_ISL_194143	South America	Brazil
A/Brazil/71886/2015	EPI_ISL_212962	South America	Brazil
A/Brazil/7588/2015	EPI_ISL_201250	South America	Brazil
A/Brazil/78870/2015	EPI_ISL_219083	South America	Brazil
A/Brazil/8004/2015	EPI_ISL_194969	South America	Brazil
A/Brazil/8433/2015	EPI_ISL_200671	South America	Brazil
A/Brazil/8438/2015	EPI_ISL_193339	South America	Brazil
A/Brazil/8925/2015	EPI_ISL_200676	South America	Brazil
A/Brazil/9056/2015	EPI_ISL_193314	South America	Brazil
A/Brazil/9492/2015	EPI_ISL_193340	South America	Brazil
A/Brazil/9517/2015	EPI_ISL_193342	South America	Brazil
A/Brazil/96/2015	EPI_ISL_195902	South America	Brazil
A/Brazil/9850/2015	EPI_ISL_200672	South America	Brazil
A/Brazil/9879/2014	EPI_ISL_168114	South America	Brazil
A/Callao/IPE00830/2012	EPI_ISL_235309	South America	Peru
A/Cambara do Sul/LACENRS-1939/2015	EPI_ISL_263253	South America	Brazil
A/Cambara do Sul/LACENRS-2049/2015	EPI_ISL_263169	South America	Brazil

A/Canoas/LACENRS-1283/2015	EPI_ISL_263142	South America	Brazil
A/Canoas/LACENRS-1317/2014	EPI_ISL_263145	South America	Brazil
A/Canoas/LACENRS-1660/2014	EPI_ISL_263140	South America	Brazil
A/Canoas/LACENRS-1793/2015	EPI_ISL_263250	South America	Brazil
A/Canoas/LACENRS-773/2015	EPI_ISL_263228	South America	Brazil
A/Colombia/1297/2016	EPI_ISL_242694	South America	Colombia
A/Colombia/1368/2016	EPI_ISL_242695	South America	Colombia
A/Colombia/1373/2016	EPI_ISL_242696	South America	Colombia
A/Colombia/1408/2016	EPI_ISL_242697	South America	Colombia
A/Colombia/235/2015	EPI_ISL_199509	South America	Colombia
A/Colombia/241/2015	EPI_ISL_199513	South America	Colombia
A/Colombia/2473/2015	EPI_ISL_179012	South America	Colombia
A/Colombia/4352/2015	EPI_ISL_179013	South America	Colombia
A/Colombia/4468/2015	EPI_ISL_179011	South America	Colombia
A/Colombia/5215/2015	EPI_ISL_199516	South America	Colombia
A/Colombia/5364/2015	EPI_ISL_199511	South America	Colombia
A/Colombia/5402/2015	EPI_ISL_199508	South America	Colombia
A/Colombia/5433/2015	EPI_ISL_201208	South America	Colombia
A/Colombia/5438/2015	EPI_ISL_199510	South America	Colombia
A/Colombia/5614/2015	EPI_ISL_195896	South America	Colombia
A/Colombia/5615/2015	EPI_ISL_195899	South America	Colombia
A/Colombia/6276/2015	EPI_ISL_212051	South America	Colombia
A/Colombia/6308/2015	EPI_ISL_212052	South America	Colombia
A/Colombia/6352/2015	EPI_ISL_220284	South America	Colombia
A/Colombia/6372/2015	EPI_ISL_214526	South America	Colombia
A/Colombia/6438/2015	EPI_ISL_212974	South America	Colombia
A/Colombia/6443/2015	EPI_ISL_212975	South America	Colombia
A/Colombia/6825/2015	EPI_ISL_212976	South America	Colombia
A/Colombia/6844/2015	EPI_ISL_212977	South America	Colombia
A/Colombia/6855/2015	EPI_ISL_214527	South America	Colombia
A/Colombia/6860/2015	EPI_ISL_215254	South America	Colombia
A/Colombia/7113/2015	EPI_ISL_212978	South America	Colombia
A/Colombia/7207/2015	EPI_ISL_212053	South America	Colombia
A/Colombia/7208/2015	EPI_ISL_212054	South America	Colombia
A/Colombia/9773/2016	EPI_ISL_234038	South America	Colombia
A/Concepcion/75466/2015	EPI_ISL_206116	South America	Chile
A/Cruz Alta/LACENRS-2045/2014	EPI_ISL_263268	South America	Brazil
A/Cruz Alta/LACENRS-2623/2014	EPI_ISL_263223	South America	Brazil
A/Ecuador/1372/2016	EPI_ISL_232553	South America	Ecuador

A/Ecuador/1374/2016	EPI_ISL_232542	South America	Ecuador
A/Ecuador/1668/2015	EPI_ISL_194962	South America	Ecuador
A/Ecuador/1670/2015	EPI_ISL_194961	South America	Ecuador
A/Ecuador/1673/2015	EPI_ISL_197496	South America	Ecuador
A/Ecuador/1695/2015	EPI_ISL_200682	South America	Ecuador
A/Ecuador/1845/2015	EPI_ISL_200684	South America	Ecuador
A/Ecuador/220/2016	EPI_ISL_232989	South America	Ecuador
A/Ecuador/2369/2015	EPI_ISL_195876	South America	Ecuador
A/Ecuador/2384/2015	EPI_ISL_194960	South America	Ecuador
A/Ecuador/2404/2015	EPI_ISL_200680	South America	Ecuador
A/Ecuador/2495/2016	EPI_ISL_232986	South America	Ecuador
A/Ecuador/2673/2016	EPI_ISL_232988	South America	Ecuador
A/Ecuador/572/2015	EPI_ISL_200681	South America	Ecuador
A/Ecuador/821/2015	EPI_ISL_200683	South America	Ecuador
A/Farroupilha/LACENRS-1297/2014	EPI_ISL_263222	South America	Brazil
A/French Guiana/5020/2015	EPI_ISL_205629	South America	French Guiana
A/French Guiana/6101/2015	EPI_ISL_201229	South America	French Guiana
A/French Guiana/8217/2015	EPI_ISL_201235	South America	French Guiana
A/French Guiana/9189/2015	EPI_ISL_201236	South America	French Guiana
A/Gorbea/75876/2015	EPI_ISL_207393	South America	Chile
A/Guyane/2773/2016	EPI_ISL_238145	South America	French Guiana
A/Guyane/2774/2016	EPI_ISL_236649	South America	French Guiana
A/Guyane/2776/2016	EPI_ISL_236651	South America	French Guiana
A/Guyane/2777/2016	EPI_ISL_238146	South America	French Guiana
A/Guyane/2780/2016	EPI_ISL_237267	South America	French Guiana
A/Guyane/2782/2016	EPI_ISL_236652	South America	French Guiana
A/Guyane/501/2016	EPI_ISL_249963	South America	French Guiana
A/Guyane/590/2016	EPI_ISL_249969	South America	French Guiana
A/Guyane/601/2016	EPI_ISL_249970	South America	French Guiana
A/ilopolis/LACENRS-1322/2014	EPI_ISL_263298	South America	Brazil
A/Iquique/62331/2014	EPI_ISL_171353	South America	Chile
A/Iquitos/FPI002788/2011	EPI_ISL_235298	South America	Peru
A/Linares/71226/2015	EPI_ISL_207402	South America	Chile
A/Novo Hamburgo/LACENRS-201/2011	EPI_ISL_263190	South America	Brazil
A/Para/134244-IEC/2015	EPI_ISL_200700	South America	Brazil
A/Para/134324-IEC/2015	EPI_ISL_200701	South America	Brazil
A/Para/134473-IEC/2015	EPI_ISL_200702	South America	Brazil
A/Para/134575-IEC/2015	EPI_ISL_200703	South America	Brazil
A/Para/134701-IEC/2015	EPI_ISL_200706	South America	Brazil

A/Paraguay/0049/2014	EPI_ISL_167947	South America	Paraguay
A/Paraguay/0094/2014	EPI_ISL_171388	South America	Paraguay
A/Paraguay/0095/2014	EPI_ISL_167948	South America	Paraguay
A/Paraguay/0097/2014	EPI_ISL_191036	South America	Paraguay
A/Paraguay/3144/2014	EPI_ISL_172529	South America	Paraguay
A/Paraguay/3371/2015	EPI_ISL_197275	South America	Paraguay
A/Paraguay/3585/2015	EPI_ISL_197273	South America	Paraguay
A/Paraguay/4413/2014	EPI_ISL_172771	South America	Paraguay
A/Paraguay/5554/2015	EPI_ISL_197277	South America	Paraguay
A/Paraguay/5821/2015	EPI_ISL_208607	South America	Paraguay
A/Paraguay/6248/2015	EPI_ISL_197274	South America	Paraguay
A/Paraguay/6991/2015	EPI_ISL_197276	South America	Paraguay
A/Paraiba/143404-IEC/2016	EPI_ISL_247962	South America	Brazil
A/Parana/87/2014	EPI_ISL_166797	South America	Brazil
A/Passo Fundo/LACENRS-1533/2013	EPI_ISL_263271	South America	Brazil
A/Passo Fundo/LACENRS-1854/2015	EPI_ISL_263376	South America	Brazil
A/Pelotas/LACENRS-1787/2015	EPI_ISL_263265	South America	Brazil
A/Pernambuco/135596-IEC/2015	EPI_ISL_203424	South America	Brazil
A/Pernambuco/135597-IEC/2015	EPI_ISL_203425	South America	Brazil
A/Pernambuco/136136-IEC/2015	EPI_ISL_203426	South America	Brazil
A/Peru/0216/2016	EPI_ISL_239673	South America	Peru
A/Peru/1216/2016	EPI_ISL_238650	South America	Peru
A/Peru/1416/2016	EPI_ISL_239674	South America	Peru
A/Peru/27/2015	EPI_ISL_192696	South America	Peru
A/Peru/2716/2016	EPI_ISL_238655	South America	Peru
A/Peru/28/2015	EPI_ISL_192703	South America	Peru
A/Peru/30/2015	EPI_ISL_192697	South America	Peru
A/Peru/3216/2016	EPI_ISL_238656	South America	Peru
A/Peru/34/2015	EPI_ISL_193334	South America	Peru
A/Peru/36/2015	EPI_ISL_193335	South America	Peru
A/Peru/37/2015	EPI_ISL_193336	South America	Peru
A/Peru/3916/2016	EPI_ISL_239675	South America	Peru
A/Peru/5116/2016	EPI_ISL_230357	South America	Peru
A/Peru/61016/2016	EPI_ISL_238654	South America	Peru
A/Peru/6116/2016	EPI_ISL_230356	South America	Peru
A/Peru/65116/2016	EPI_ISL_242716	South America	Peru
A/Peru/69/2015	EPI_ISL_203428	South America	Peru
A/Peru/6915/2015	EPI_ISL_202391	South America	Peru
A/Peru/71/2015	EPI_ISL_207389	South America	Peru

A/Peru/72/2015	EPI_ISL_207390	South America	Peru
A/Peru/81016/2016	EPI_ISL_239676	South America	Peru
A/Peru/8116/2016	EPI_ISL_238652	South America	Peru
A/Peru/8316/2016	EPI_ISL_240144	South America	Peru
A/Peru/9016/2016	EPI_ISL_230358	South America	Peru
A/Peru/PER002/2010	EPI_ISL_152097	South America	Peru
A/Peru/PER005/2010	EPI_ISL_152148	South America	Peru
A/Peru/PER006/2011	EPI_ISL_152149	South America	Peru
A/Peru/PER008/2010	EPI_ISL_152151	South America	Peru
A/Peru/PER009/2010	EPI_ISL_152152	South America	Peru
A/Peru/PER011/2010	EPI_ISL_152154	South America	Peru
A/Peru/PER014/2011	EPI_ISL_152157	South America	Peru
A/Peru/PER015/2010	EPI_ISL_152158	South America	Peru
A/Peru/PER016/2011	EPI_ISL_152159	South America	Peru
A/Peru/PER021/2010	EPI_ISL_152164	South America	Peru
A/Peru/PER023/2010	EPI_ISL_152166	South America	Peru
A/Peru/PER024/2010	EPI_ISL_152167	South America	Peru
A/Peru/PER025/2010	EPI_ISL_152168	South America	Peru
A/Peru/PER026/2010	EPI_ISL_152169	South America	Peru
A/Peru/PER027/2011	EPI_ISL_152170	South America	Peru
A/Peru/PER028/2011	EPI_ISL_152171	South America	Peru
A/Peru/PER031/2012	EPI_ISL_152174	South America	Peru
A/Peru/PER032/2010	EPI_ISL_152175	South America	Peru
A/Peru/PER033/2010	EPI_ISL_152176	South America	Peru
A/Peru/PER035/2010	EPI_ISL_152178	South America	Peru
A/Peru/PER036/2011	EPI_ISL_152179	South America	Peru
A/Peru/PER038/2010	EPI_ISL_152181	South America	Peru
A/Peru/PER043/2011	EPI_ISL_152187	South America	Peru
A/Peru/PER044/2011	EPI_ISL_152188	South America	Peru
A/Peru/PER046/2010	EPI_ISL_152190	South America	Peru
A/Peru/PER047/2011	EPI_ISL_152192	South America	Peru
A/Peru/PER050/2010	EPI_ISL_152195	South America	Peru
A/Peru/PER051/2012	EPI_ISL_152245	South America	Peru
A/Peru/PER053/2010	EPI_ISL_152247	South America	Peru
A/Peru/PER055/2011	EPI_ISL_152249	South America	Peru
A/Peru/PER056/2011	EPI_ISL_152250	South America	Peru
A/Peru/PER061/2011	EPI_ISL_152255	South America	Peru
A/Peru/PER062/2010	EPI_ISL_152256	South America	Peru
A/Peru/PER063/2012	EPI_ISL_152257	South America	Peru

A/Peru/PER064/2010	EPI_ISL_152258	South America	Peru
A/Peru/PER066/2011	EPI_ISL_152260	South America	Peru
A/Peru/PER067/2011	EPI_ISL_152261	South America	Peru
A/Peru/PER068/2010	EPI_ISL_152262	South America	Peru
A/Peru/PER069/2011	EPI_ISL_152263	South America	Peru
A/Peru/PER071/2010	EPI_ISL_152265	South America	Peru
A/Peru/PER074/2010	EPI_ISL_152268	South America	Peru
A/Peru/PER075/2010	EPI_ISL_152269	South America	Peru
A/Peru/PER077/2010	EPI_ISL_152271	South America	Peru
A/Peru/PER079/2010	EPI_ISL_152273	South America	Peru
A/Peru/PER081/2012	EPI_ISL_152275	South America	Peru
A/Peru/PER083/2010	EPI_ISL_152277	South America	Peru
A/Peru/PER090/2010	EPI_ISL_152284	South America	Peru
A/Peru/PER092/2011	EPI_ISL_152285	South America	Peru
A/Peru/PER093/2010	EPI_ISL_152286	South America	Peru
A/Peru/PER094/2010	EPI_ISL_152287	South America	Peru
A/Peru/PER096/2012	EPI_ISL_152289	South America	Peru
A/Peru/PER097/2011	EPI_ISL_152290	South America	Peru
A/Peru/PER101/2010	EPI_ISL_152344	South America	Peru
A/Peru/PER102/2012	EPI_ISL_152345	South America	Peru
A/Peru/PER108/2012	EPI_ISL_152351	South America	Peru
A/Peru/PER113/2012	EPI_ISL_152356	South America	Peru
A/Peru/PER114/2010	EPI_ISL_152357	South America	Peru
A/Peru/PER116/2010	EPI_ISL_152359	South America	Peru
A/Peru/PER118/2011	EPI_ISL_152361	South America	Peru
A/Peru/PER119/2010	EPI_ISL_152362	South America	Peru
A/Peru/PER123/2010	EPI_ISL_152366	South America	Peru
A/Peru/PER124/2012	EPI_ISL_152367	South America	Peru
A/Peru/PER125/2010	EPI_ISL_152368	South America	Peru
A/Peru/PER127/2010	EPI_ISL_152369	South America	Peru
A/Peru/PER128/2010	EPI_ISL_152370	South America	Peru
A/Peru/PER129/2010	EPI_ISL_152371	South America	Peru
A/Peru/PER130/2011	EPI_ISL_152372	South America	Peru
A/Peru/PER132/2011	EPI_ISL_152374	South America	Peru
A/Peru/PER135/2010	EPI_ISL_152377	South America	Peru
A/Peru/PER136/2011	EPI_ISL_152378	South America	Peru
A/Peru/PER138/2010	EPI_ISL_152380	South America	Peru
A/Peru/PER139/2010	EPI_ISL_152381	South America	Peru
A/Peru/PER142/2011	EPI_ISL_152384	South America	Peru

A/Peru/PER144/2012	EPI_ISL_152386	South America	Peru
A/Peru/PER145/2010	EPI_ISL_152387	South America	Peru
A/Peru/PER147/2010	EPI_ISL_152389	South America	Peru
A/Peru/PER148/2010	EPI_ISL_152390	South America	Peru
A/Peru/PER157/2010	EPI_ISL_152433	South America	Peru
A/Peru/PER161/2011	EPI_ISL_152437	South America	Peru
A/Peru/PER165/2010	EPI_ISL_152441	South America	Peru
A/Peru/PER170/2010	EPI_ISL_152446	South America	Peru
A/Peru/PER171/2010	EPI_ISL_152447	South America	Peru
A/Peru/PER173/2010	EPI_ISL_152449	South America	Peru
A/Peru/PER178/2010	EPI_ISL_152454	South America	Peru
A/Peru/PER180/2010	EPI_ISL_152456	South America	Peru
A/Peru/PER182/2010	EPI_ISL_152458	South America	Peru
A/Peru/PER185/2011	EPI_ISL_152461	South America	Peru
A/Peru/PER186/2012	EPI_ISL_152499	South America	Peru
A/Peru/PER187/2011	EPI_ISL_152500	South America	Peru
A/Peru/PER188/2010	EPI_ISL_152501	South America	Peru
A/Peru/PER192/2010	EPI_ISL_152505	South America	Peru
A/Peru/PER193/2010	EPI_ISL_152506	South America	Peru
A/Peru/PER196/2010	EPI_ISL_152509	South America	Peru
A/Peru/PER197/2011	EPI_ISL_152510	South America	Peru
A/Peru/PER201/2010	EPI_ISL_152838	South America	Peru
A/Peru/PER203/2011	EPI_ISL_152570	South America	Peru
A/Peru/PER205/2011	EPI_ISL_152572	South America	Peru
A/Peru/PER207/2010	EPI_ISL_152574	South America	Peru
A/Peru/PER210/2010	EPI_ISL_152577	South America	Peru
A/Peru/PER211/2010	EPI_ISL_152578	South America	Peru
A/Peru/PER212/2010	EPI_ISL_152579	South America	Peru
A/Peru/PER214/2010	EPI_ISL_152581	South America	Peru
A/Peru/PER218/2010	EPI_ISL_152585	South America	Peru
A/Peru/PER220/2010	EPI_ISL_152587	South America	Peru
A/Peru/PER222/2012	EPI_ISL_152589	South America	Peru
A/Peru/PER224/2010	EPI_ISL_152591	South America	Peru
A/Peru/PER225/2010	EPI_ISL_152592	South America	Peru
A/Peru/PER228/2010	EPI_ISL_152595	South America	Peru
A/Peru/PER229/2010	EPI_ISL_152596	South America	Peru
A/Peru/PER232/2012	EPI_ISL_152599	South America	Peru
A/Peru/PER241/2010	EPI_ISL_152607	South America	Peru
A/Peru/PER242/2010	EPI_ISL_152608	South America	Peru

A/Peru/PER246/2010	EPI_ISL_152612	South America	Peru
A/Peru/PER247/2011	EPI_ISL_152613	South America	Peru
A/Peru/PER248/2010	EPI_ISL_152614	South America	Peru
A/Peru/PER258/2010	EPI_ISL_152645	South America	Peru
A/Peru/PER259/2010	EPI_ISL_152646	South America	Peru
A/Peru/PER260/2012	EPI_ISL_152647	South America	Peru
A/Peru/PER263/2010	EPI_ISL_152649	South America	Peru
A/Peru/PER265/2011	EPI_ISL_152651	South America	Peru
A/Peru/PER266/2010	EPI_ISL_152652	South America	Peru
A/Peru/PER267/2010	EPI_ISL_152653	South America	Peru
A/Peru/PER268/2011	EPI_ISL_152654	South America	Peru
A/Peru/PER269/2011	EPI_ISL_152655	South America	Peru
A/Peru/PER270/2010	EPI_ISL_152656	South America	Peru
A/Peru/PER273/2011	EPI_ISL_152659	South America	Peru
A/Peru/PER274/2010	EPI_ISL_152660	South America	Peru
A/Peru/PER277/2010	EPI_ISL_152663	South America	Peru
A/Peru/PER279/2010	EPI_ISL_152683	South America	Peru
A/Peru/PER280/2012	EPI_ISL_152699	South America	Peru
A/Peru/PER281/2011	EPI_ISL_152684	South America	Peru
A/Peru/PER284/2011	EPI_ISL_152687	South America	Peru
A/Peru/PER287/2011	EPI_ISL_152690	South America	Peru
A/Peru/PER288/2010	EPI_ISL_152691	South America	Peru
A/Peru/PER289/2011	EPI_ISL_152692	South America	Peru
A/Peru/PER290/2011	EPI_ISL_152693	South America	Peru
A/Peru/PER294/2010	EPI_ISL_152696	South America	Peru
A/Peru/PER298/2011	EPI_ISL_152839	South America	Peru
A/Peru/PER299/2010	EPI_ISL_152840	South America	Peru
A/Peru/PER308/2010	EPI_ISL_152742	South America	Peru
A/Peru/PER309/2012	EPI_ISL_152743	South America	Peru
A/Peru/PER310/2010	EPI_ISL_152744	South America	Peru
A/Peru/PER311/2010	EPI_ISL_152745	South America	Peru
A/Peru/PER314/2012	EPI_ISL_152748	South America	Peru
A/Peru/PER315/2010	EPI_ISL_152749	South America	Peru
A/Peru/PER316/2012	EPI_ISL_152750	South America	Peru
A/Peru/PER318/2010	EPI_ISL_152752	South America	Peru
A/Peru/PER320/2010	EPI_ISL_152754	South America	Peru
A/Peru/PER321/2010	EPI_ISL_152755	South America	Peru
A/Peru/PER323/2010	EPI_ISL_152757	South America	Peru
A/Peru/PER324/2011	EPI_ISL_152758	South America	Peru

A/Peru/PER328/2011	EPI_ISL_152762	South America	Peru
A/Peru/PER330/2010	EPI_ISL_152764	South America	Peru
A/Peru/PER332/2010	EPI_ISL_152766	South America	Peru
A/Peru/PER334/2011	EPI_ISL_152768	South America	Peru
A/Peru/PER337/2011	EPI_ISL_152771	South America	Peru
A/Peru/PER338/2010	EPI_ISL_152772	South America	Peru
A/Peru/PER341/2011	EPI_ISL_152775	South America	Peru
A/Peru/PER342/2010	EPI_ISL_152776	South America	Peru
A/Peru/PER345/2011	EPI_ISL_152809	South America	Peru
A/Peru/PER346/2011	EPI_ISL_152837	South America	Peru
A/Peru/PER351/2010	EPI_ISL_152813	South America	Peru
A/Peru/PER354/2012	EPI_ISL_152816	South America	Peru
A/Peru/PER355/2011	EPI_ISL_152817	South America	Peru
A/Peru/PER357/2010	EPI_ISL_152819	South America	Peru
A/Peru/PER358/2012	EPI_ISL_152820	South America	Peru
A/Peru/PER359/2012	EPI_ISL_152821	South America	Peru
A/Peru/PER361/2010	EPI_ISL_152823	South America	Peru
A/Peru/PER362/2011	EPI_ISL_152824	South America	Peru
A/Peru/PER365/2010	EPI_ISL_152827	South America	Peru
A/Peru/PER369/2010	EPI_ISL_152829	South America	Peru
A/Peru/PER370/2010	EPI_ISL_152830	South America	Peru
A/Peru/PER371/2012	EPI_ISL_152831	South America	Peru
A/Peru/PER374/2011	EPI_ISL_152834	South America	Peru
A/Peru/PER379/2010	EPI_ISL_152464	South America	Peru
A/Peru/PER380/2010	EPI_ISL_152465	South America	Peru
A/Peru/PER381/2010	EPI_ISL_152466	South America	Peru
A/Peru/PER384/2012	EPI_ISL_152469	South America	Peru
A/Peru/PER386/2010	EPI_ISL_152471	South America	Peru
A/Peru/PER389/2012	EPI_ISL_152498	South America	Peru
A/Peru/PER390/2010	EPI_ISL_152487	South America	Peru
A/Peru/PER393/2010	EPI_ISL_152490	South America	Peru
A/Peru/PER394/2011	EPI_ISL_152491	South America	Peru
A/Peru/PER395/2011	EPI_ISL_152492	South America	Peru
A/Peru/PER397/2011	EPI_ISL_152494	South America	Peru
A/Peru/PER399/2012	EPI_ISL_152496	South America	Peru
A/Peru/PER400/2012	EPI_ISL_152497	South America	Peru
A/Porto Alegre/LACENRS-1013/2016	EPI_ISL_263257	South America	Brazil
A/Porto Alegre/LACENRS-1030/2015	EPI_ISL_263269	South America	Brazil
A/Porto Alegre/LACENRS-1075/2015	EPI_ISL_263242	South America	Brazil

A/Porto Alegre/LACENRS-1112/2015	EPI_ISL_263230	South America	Brazil
A/Porto Alegre/LACENRS-1155/2015	EPI_ISL_263374	South America	Brazil
A/Porto Alegre/LACENRS-1351/2014	EPI_ISL_263251	South America	Brazil
A/Porto Alegre/LACENRS-1406/2014	EPI_ISL_263170	South America	Brazil
A/Porto Alegre/LACENRS-1447/2014	EPI_ISL_263125	South America	Brazil
A/Porto Alegre/LACENRS-1738/2015	EPI_ISL_263137	South America	Brazil
A/Porto Alegre/LACENRS-1887/2015	EPI_ISL_263161	South America	Brazil
A/Porto Alegre/LACENRS-1969/2015	EPI_ISL_263234	South America	Brazil
A/Porto Alegre/LACENRS-2021/2014	EPI_ISL_263124	South America	Brazil
A/Porto Alegre/LACENRS-2232/2014	EPI_ISL_263259	South America	Brazil
A/Porto Alegre/LACENRS-2376/2014	EPI_ISL_263247	South America	Brazil
A/Porto Alegre/LACENRS-557/2011	EPI_ISL_263132	South America	Brazil
A/Porto Alegre/LACENRS-820/2015	EPI_ISL_263174	South America	Brazil
A/Porto Alegre/LACENRS-846/2015	EPI_ISL_263203	South America	Brazil
A/Porto Alegre/LACENRS-921/2015	EPI_ISL_263302	South America	Brazil
A/Pucallpa/FPU00363/2011	EPI_ISL_235302	South America	Peru
A/Pucallpa/FPU00370/2011	EPI_ISL_235303	South America	Peru
A/Rio Grande Do Norte/134592-IEC/2015	EPI_ISL_200704	South America	Brazil
A/Rio Grande Do Norte/134696-IEC/2015	EPI_ISL_200705	South America	Brazil
A/Rio Grande Do Norte/135219-IEC/2015	EPI_ISL_201224	South America	Brazil
A/Rio Grande Do Norte/135497-IEC/2015	EPI_ISL_201226	South America	Brazil
A/Rio Grande do Sul/23/2014	EPI_ISL_166794	South America	Brazil
A/Roraima/141969-IEC/2016	EPI_ISL_233003	South America	Brazil
A/Roraima/143199-IEC/2016	EPI_ISL_247961	South America	Brazil
A/Roraima/144096-IEC/2016	EPI_ISL_247963	South America	Brazil
A/Roraima/144238-IEC/2016	EPI_ISL_247964	South America	Brazil
A/Roraima/144714-IEC/2016	EPI_ISL_247965	South America	Brazil
A/Santa Cruz do Sul/LACENRS-1625/2014	EPI_ISL_263136	South America	Brazil
A/Santa Cruz do Sul/LACENRS-913/2011	EPI_ISL_263195	South America	Brazil
A/Santa Maria/LACENRS-231/2011	EPI_ISL_263256	South America	Brazil
A/Santiago/33417/2015	EPI_ISL_193313	South America	Chile
A/Santiago/35385/2015	EPI_ISL_194975	South America	Chile
A/Santiago/37245/2015	EPI_ISL_194971	South America	Chile
A/Santiago/39170/2015	EPI_ISL_193318	South America	Chile
A/Santiago/40992/2015	EPI_ISL_194972	South America	Chile
A/Santiago/42575/2015	EPI_ISL_194973	South America	Chile
A/Santiago/44139/2015	EPI_ISL_194974	South America	Chile
A/Santiago/68839/2014	EPI_ISL_172778	South America	Chile
A/Santiago/70123/2014	EPI_ISL_171369	South America	Chile

A/Santiago/70910/2015	EPI_ISL_207407	South America	Chile
A/Suriname/1665/2016	EPI_ISL_253049	South America	Suriname
A/Suriname/1683/2016	EPI_ISL_253050	South America	Suriname
A/Suriname/1693/2016	EPI_ISL_253051	South America	Suriname
A/Suriname/1716/2016	EPI_ISL_253052	South America	Suriname
A/Talca/14380/2016	EPI_ISL_225093	South America	Chile
A/Talca/79797/2015	EPI_ISL_207456	South America	Chile
A/Temuco/50233/2016	EPI_ISL_232534	South America	Chile
A/Temuco/75349/2015	EPI_ISL_206115	South America	Chile
A/Uruguay/122/2015	EPI_ISL_199517	South America	Uruguay
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A/Uruguay/44/2015	EPI_ISL_199506	South America	Uruguay
A/Uruguay/54/2015	EPI_ISL_199521	South America	Uruguay
A/Uruguay/55/2015	EPI_ISL_199522	South America	Uruguay
A/Uruguay/86/2015	EPI_ISL_199504	South America	Uruguay
A/Valparaiso/42142/2015	EPI_ISL_194979	South America	Chile
A/Valparaiso/50516/2016	EPI_ISL_232535	South America	Chile
A/Valparaiso/51089/2016	EPI_ISL_232537	South America	Chile
A/Venezuela/07/2014	EPI_ISL_172735	South America	Venezuela
A/Venezuela/13/2016	EPI_ISL_237365	South America	Venezuela
A/Viamao/LACENRS-733/2014	EPI_ISL_263237	South America	Brazil
A/Viamao/LACENRS-974/2015	EPI_ISL_263252	South America	Brazil
A/American Samoa/4786/2013	EPI_ISL_145508	Oceania	American Samoa
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A/Brisbane/1/2013	EPI_ISL_288262	Oceania	Australia
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A/Brisbane/119/2015	EPI_ISL_288043	Oceania	Australia
A/Brisbane/12/2015	EPI_ISL_288148	Oceania	Australia
A/Brisbane/127/2015	EPI_ISL_287976	Oceania	Australia
A/Brisbane/134/2015	EPI_ISL_287981	Oceania	Australia

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A/Brisbane/140/2015	EPI_ISL_287983	Oceania	Australia
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A/Brisbane/16/2013	EPI_ISL_288245	Oceania	Australia
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A/Brisbane/21/2013	EPI_ISL_288246	Oceania	Australia
A/Brisbane/22/2015	EPI_ISL_288146	Oceania	Australia
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A/Brisbane/318/2016	EPI_ISL_269294	Oceania	Australia
A/Brisbane/324/2016	EPI_ISL_288819	Oceania	Australia
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A/BRISBANE/395/2011	EPI_ISL_106863	Oceania	Australia
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A/Brisbane/6/2012	EPI_ISL_288817	Oceania	Australia
A/Brisbane/61/2012	EPI_ISL_288387	Oceania	Australia

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A/Canberra/93/2016	EPI_ISL_288849	Oceania	Australia
A/CHRISTCHURCH/503/2012	EPI_ISL_128643	Oceania	New Zealand
A/Christchurch/505/2016	EPI_ISL_237834	Oceania	New Zealand
A/CHRISTCHURCH/516/2012	EPI_ISL_128644	Oceania	New Zealand
A/Darwin/1000/2015	EPI_ISL_287834	Oceania	Australia
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A/Darwin/1006/2016	EPI_ISL_289029	Oceania	Australia
A/Dunedin/3/2016	EPI_ISL_232818	Oceania	New Zealand
A/Fiji/02/2015	EPI_ISL_194166	Oceania	Fiji
A/FIJI/1/2014	EPI_ISL_166142	Oceania	Fiji
A/Fiji/7/2015	EPI_ISL_219049	Oceania	Fiji
A/GOROKA/5/2011	EPI_ISL_106847	Oceania	New Zealand
A/GOROKA/5/2012	EPI_ISL_122579	Oceania	New Zealand
A/HAWKES BAY/1/2013	EPI_ISL_161323	Oceania	New Zealand
A/NAURU/5/2011	EPI_ISL_95078	Oceania	Nauru
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A/New Zealand/0635/2016	EPI_ISL_235061	Oceania	New Zealand
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A/New Zealand/0779/2016	EPI_ISL_240115	Oceania	New Zealand
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A/New Zealand/0879/2016	EPI_ISL_235070	Oceania	New Zealand
A/New Zealand/0888/2016	EPI_ISL_237369	Oceania	New Zealand
A/New Zealand/0889/2016	EPI_ISL_240123	Oceania	New Zealand
A/New Zealand/0977/2016	EPI_ISL_240321	Oceania	New Zealand
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A/New Zealand/1017/2016	EPI_ISL_240314	Oceania	New Zealand
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A/New Zealand/562/2015	EPI_ISL_197508	Oceania	New Zealand
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A/Newcastle/64/2015	EPI_ISL_226255	Oceania	Australia

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A/Palau/6759/2014	EPI_ISL_164404	Oceania	Palau
A/Palau/6775/2014	EPI_ISL_167865	Oceania	Palau
A/Perth/113/2015	EPI_ISL_287949	Oceania	Australia
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A/South Auckland/23/2016	EPI_ISL_232811	Oceania	New Zealand
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A/South Australia/1005/2014	EPI_ISL_288208	Oceania	Australia

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A/South Australia/9/2015	EPI_ISL_288165	Oceania	Australia
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A/Townsville/51/2016	EPI_ISL_288830	Oceania	Australia
A/Victoria/1000/2015	EPI_ISL_219035	Oceania	Australia
A/Victoria/1002/2012	EPI_ISL_288383	Oceania	Australia
A/Victoria/1002A/2012	EPI_ISL_288254	Oceania	Australia
A/Victoria/1003/2012	EPI_ISL_288359	Oceania	Australia
A/Victoria/1006/2015	EPI_ISL_287861	Oceania	Australia
A/Victoria/1012/2014	EPI_ISL_288176	Oceania	Australia
A/VICTORIA/103/2011	EPI_ISL_99771	Oceania	Australia
A/Victoria/109/2016	EPI_ISL_288863	Oceania	Australia
A/Victoria/113/2012	EPI_ISL_288385	Oceania	Australia
A/Victoria/115/2014	EPI_ISL_288158	Oceania	Australia
A/Victoria/120/2012	EPI_ISL_288386	Oceania	Australia
A/Victoria/123/2016	EPI_ISL_288864	Oceania	Australia
A/Victoria/142/2012	EPI_ISL_288377	Oceania	Australia
A/Victoria/147/2012	EPI_ISL_288378	Oceania	Australia
A/Victoria/148/2012	EPI_ISL_288374	Oceania	Australia
A/Victoria/16/2015	EPI_ISL_287992	Oceania	Australia
A/Victoria/173/2012	EPI_ISL_288372	Oceania	Australia
A/Victoria/175/2012	EPI_ISL_288373	Oceania	Australia
A/Victoria/184/2012	EPI_ISL_288366	Oceania	Australia
A/Victoria/187/2012	EPI_ISL_288370	Oceania	Australia
A/Victoria/19/2015	EPI_ISL_287943	Oceania	Australia
A/Victoria/2074/2016	EPI_ISL_289072	Oceania	Australia
A/Victoria/2079/2016	EPI_ISL_289053	Oceania	Australia
A/Victoria/21/2015	EPI_ISL_287944	Oceania	Australia
A/Victoria/2102/2016	EPI_ISL_289064	Oceania	Australia
A/Victoria/2111/2016	EPI_ISL_289071	Oceania	Australia
A/Victoria/213/2012	EPI_ISL_288361	Oceania	Australia
A/Victoria/2502/2015	EPI_ISL_287991	Oceania	Australia
A/Victoria/27/2012	EPI_ISL_288802	Oceania	Australia
A/Victoria/27/2014	EPI_ISL_288206	Oceania	Australia
A/Victoria/3/2012	EPI_ISL_288811	Oceania	Australia
A/Victoria/3009/2015	EPI_ISL_287864	Oceania	Australia
A/Victoria/3015/2015	EPI_ISL_287883	Oceania	Australia
A/Victoria/3070/2015	EPI_ISL_287929	Oceania	Australia
A/Victoria/3079/2015	EPI_ISL_287894	Oceania	Australia
A/Victoria/3085/2015	EPI_ISL_287867	Oceania	Australia
A/Victoria/346/2012	EPI_ISL_288394	Oceania	Australia

A/Victoria/361/2011	EPI_ISL_101506	Oceania	Australia
A/Victoria/43/2012	EPI_ISL_288401	Oceania	Australia
A/Victoria/448/2012	EPI_ISL_288379	Oceania	Australia
A/Victoria/50/2012	EPI_ISL_288404	Oceania	Australia
A/Victoria/503/2014	EPI_ISL_288226	Oceania	Australia
A/Victoria/503/2015	EPI_ISL_194165	Oceania	Australia
A/Victoria/504/2013	EPI_ISL_288249	Oceania	Australia
A/Victoria/505/2013	EPI_ISL_145684	Oceania	Australia
A/Victoria/5054/2014	EPI_ISL_288181	Oceania	Australia
A/VICTORIA/506/2011	EPI_ISL_94782	Oceania	Australia
A/Victoria/506/2013	EPI_ISL_152924	Oceania	Australia
A/VICTORIA/5060/2014	EPI_ISL_168962	Oceania	Australia
A/Victoria/5065/2014	EPI_ISL_288168	Oceania	Australia
A/Victoria/5075/2014	EPI_ISL_288173	Oceania	Australia
A/Victoria/508/2012	EPI_ISL_288809	Oceania	Australia
A/Victoria/508/2016	EPI_ISL_289107	Oceania	Australia
A/Victoria/51/2015	EPI_ISL_287835	Oceania	Australia
A/Victoria/519/2015	EPI_ISL_288022	Oceania	Australia
A/Victoria/523/2015	EPI_ISL_288024	Oceania	Australia
A/Victoria/527/2015	EPI_ISL_288025	Oceania	Australia
A/Victoria/528/2013	EPI_ISL_288236	Oceania	Australia
A/Victoria/528/2014	EPI_ISL_288194	Oceania	Australia
A/Victoria/53/2015	EPI_ISL_287817	Oceania	Australia
A/Victoria/535/2012	EPI_ISL_288403	Oceania	Australia
A/Victoria/542/2016	EPI_ISL_289100	Oceania	Australia
A/Victoria/546/2016	EPI_ISL_289095	Oceania	Australia
A/Victoria/55/2015	EPI_ISL_287847	Oceania	Australia
A/Victoria/576/2016	EPI_ISL_289076	Oceania	Australia
A/Victoria/589/2016	EPI_ISL_289069	Oceania	Australia
A/Victoria/600/2016	EPI_ISL_289060	Oceania	Australia
A/Victoria/63/2015	EPI_ISL_287849	Oceania	Australia
A/Victoria/63/2016	EPI_ISL_289061	Oceania	Australia
A/Victoria/64/2015	EPI_ISL_287848	Oceania	Australia
A/Victoria/640/2013	EPI_ISL_288241	Oceania	Australia
A/Victoria/641/2012	EPI_ISL_288375	Oceania	Australia
A/Victoria/660/2016	EPI_ISL_288837	Oceania	Australia
A/Victoria/664/2015	EPI_ISL_209046	Oceania	Australia
A/Victoria/668/2016	EPI_ISL_288845	Oceania	Australia
A/Victoria/670/2016	EPI_ISL_288838	Oceania	Australia

A/Victoria/673/2014	EPI_ISL_288171	Oceania	Australia
A/Victoria/692/2012	EPI_ISL_288376	Oceania	Australia
A/Victoria/7/2012	EPI_ISL_288797	Oceania	Australia
A/Victoria/700/2013	EPI_ISL_288261	Oceania	Australia
A/Victoria/710/2013	EPI_ISL_288260	Oceania	Australia
A/Victoria/723/2012	EPI_ISL_288380	Oceania	Australia
A/Victoria/78/2012	EPI_ISL_288405	Oceania	Australia
A/VICTORIA/802/2012	EPI_ISL_122600	Oceania	Australia
A/Victoria/806/2014	EPI_ISL_288224	Oceania	Australia
A/Victoria/820/2015	EPI_ISL_287982	Oceania	Australia
A/Victoria/837/2015	EPI_ISL_287968	Oceania	Australia
A/Victoria/84/2012	EPI_ISL_288406	Oceania	Australia
A/Victoria/853/2015	EPI_ISL_287973	Oceania	Australia
A/Victoria/87/2012	EPI_ISL_288393	Oceania	Australia
A/VICTORIA/893/2011	EPI_ISL_118588	Oceania	Australia
A/Victoria/909/2016	EPI_ISL_289077	Oceania	Australia
A/Victoria/918/2012	EPI_ISL_288356	Oceania	Australia
A/WELLINGTON/81/2014	EPI_ISL_168963	Oceania	New Zealand